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SEARCH REPORT

(54) Title: METHODS OF IDENTIFYING AGENT THAT AFFECT CLEAVAGE OF AMYLOID-β PRECURSOR PROTEIN

(57) Abstract: The present invention provides methods of identifying agents that affect the cleavage of amyloid-β precursor protein (APP) and related vectors, cells and kits, as well as agents identified by the method.

METHODS OF IDENTIFYING AGENTS THAT AFFECT CLEAVAGE OF AMYLOID-β PRECURSOR PROTEIN

SPECIFICATION

BACKGROUND OF THE INVENTION

5   Alzheimer's disease is a degenerative brain disorder that is characterized clinically by progressive loss of memory and cognitive impairment. Pathologically, the disease is characterized by lesions comprising neurofibrillary tangles, cerebrovascular amyloid deposits, and neuritic plaques. The cerebrovascular amyloid deposits and neuritic plaques contain amyloid-β peptide. The aggregation of

10   amyloid-β peptide is instrumental in the pathogenesis of Alzheimer's disease.

         Amyloid-β peptide is derived from amyloid-β precursor protein (APP). APP is a cell-surface protein with a large N-terminal extracellular sequence, a single transmembrane region (TMR) and a short C-terminal cytoplasmic tail. APP is processed by proteolysis in all cells. Initially, α- and β-secretases cleave APP at

15   defined extracellular sequences just outside of the TMR to release a large N-terminal extracellular fragment. Thereafter, γ-secretase cuts APP in the middle of the TMR to generate small extracellular peptides and a C-terminal fragment comprising half of the TMR and the full cytoplasmic tail. See, e.g., Selkoe (1998) Trends Cell Biol. 8, 447-453; Bayer et al. (1999) Mol. Psychiatry 4, 524; Haass et al. (1999) Science 286, 916-

20   919; Price et al. (1998) Ann. Rev. Gevet 32, 461-493

         Cleavage of APP by β- and γ-secretase produces the amyloid-β peptides (AP40 and AP42) implicated in the pathogeneses of Alzheimer's disease. Various methods for the diagnosis and monitoring of the disease involve assessing the cleavage of APP and detection of amyloid-β peptide. However, these methods suffer

25   from various disadvantages including the insolubility of amyloid-β peptide, cross-reactivity of antibodies against the peptide with the precursor APP, and different levels of protease activity in different body fluids.

         The γ-cleavage of APP is mediated by presenilins, intrinsic membrane proteins that may correspond to γ-secretase and that are mutated in some cases of

familial Alzheimer's disease. See, e.g., Esler et al. (2000) Nat. Cel. Biol. 2, 428-434.
Also, γ-cleavage occurs in APP-homologs that are not implicated in Alzheimer's
disease. For example, Notch proteins are membrane proteins that are also cleaved in
the middle of the TMR in a presenilin-dependent reaction. See, e.g. Ye et al. (1999)

5   Nature 398, 525-529; De Strooper et al. (1999) Nature 398, 518-522; Struhl et al.
(1999) Nature 398, 522-525. Notch proteins are cell-surface proteins involved in
intercellular signaling in which presenilin-dependent cleavage liberates a cytoplasmic
fragment that functions in nuclear transcription. Struhl et al. (2000) Mol. Cell 6, 625-
636. Sterol regulatory element binding proteins (SREPPs) are also cleaved in the

10   TMRs to generate nuclear transcription factors. Brown et al. (2000) Cell 100, 391-
398. In contrast, the physiological significance of γ-cleavage of APP, and in
particular the biological role of the cytoplasmic tail fragment, has heretofore been
unclear. In accordance with the present invention it has been discovered that the
cytoplasmic tail forms a functional complex with nuclear proteins, and that the

15   complex is a potent stimulator of transcription. The present invention thus provides
new methods for identifying agents that affect the cleavage of APP.

SUMMARY OF THE INVENTION

The present invention provides a method of identifying an agent that
affects the cleavage of APP comprising contacting a cell containing APP modified in

20   the C-terminal cytoplasmic tail to allow detection of nuclear localization with a
candidate agent and measuring nuclear localization of a C-terminal cytoplasmic
cleavage product of APP in the presence and absence of the agent.

In another embodiment, the present invention provides a method of
identifying an agent that affects the cleavage of APP comprising providing a cell

25   containing APP and a protein that interacts with the C-terminal cytoplasmic cleavage
product of APP to regulate transcription, wherein the protein is modified to allow
detection of nuclear localization of the C-terminal cytoplasmic cleavage product of
APP; contacting the cell with a candidate agent; and measuring nuclear localization of
the C-terminal cytoplasmic cleavage product of APP in the presence and absence of

30   the agent.

The invention further provides agents identified by the foregoing method, and compositions comprising the agents.

In another embodiment, the invention is directed to vectors, transfected cells and kits useful for identifying an agent that affects the cleavage of APP.

5   BRIEF DESCRIPTION OF THE DRAWINGS

Figs. 1A-C show results of Gal4-transactivation assays in PC12 cells (Fig. 1A) and HEK293 cells (Fig. 1B) and the domain structures of proteins encoded by the test plasmids (Fig. 1C). Test plasmids are identified by numbers below the bars in Figs. 1A and 1B. Luciferase activity was normalized for β-galactosidase

10   activity to control for translation efficiency. In Fig. 1A, luciferase activity was additionally normalized for the activity of cells co-transfected with Gal4 alone. Figs. 1A and 1B show results from representative experiments.

Figs. 2A-D show results of Gal4-transactivation assays (Figs. 2A-C) obtained with the constructs depicted (Fig. 2D). All bar diagrams exhibit

15   representative experiments in the cell types identified to the right of the panel.

Fig. 3 depicts an immunoblot of COS cells transfected with APP-Gal4 fusion proteins. The positions of full-length APP-Gal4, the α/β- and γ-cleavage products of APP-Gal4 (APP α/β-Gal4 and APP γ-Gal4, respectively) and the cytoplasmic tail of APP-Gal4 (APPct-Gal4) are indicated on the right. Numbers on

20   the left show positions of molecular weight markers.

Figs. 4A-C show transactivation of transcription measured with Gal4-fusion proteins and a Gal4-dependent reporter plasmid (Fig. 4A) as compared with transactivation obtained with LexA-fusion proteins and a LexA-dependent reporter plasmid (Fig. 4B). The structures of the proteins co-expressed with the

25   reporter plasmids and the control β-galactosidase vector are shown in Fig. 4C. Transcriptional activation is expressed as fold increase over transcription obtained with the DNA-binding proteins expressed alone.

Figs. 5A-E show transactivation using full length APP-Gal4 (Fig. 5A) and APP-LexA (Fig. 5B) fusion proteins co-transfected with corresponding reporter

30   plasmids and a β-galactosidase control plasmids. Various Fe65 proteins described

below the bar diagrams were co-transfected with the test and control plasmids. Transactivation is expressed as fold induction over transfection with Gal4-APP or LexA-APP alone. The domain structure of Fe65 and deletion mutants of Fe65 are shown in Fig. 5E. Figs. 5C and D show results of immunoprecipitations carried out

5   with antibodies to the myc-epitope (Fig. 5C) or to APP (Fig. 5D; PIS=preimmune serum) and analyzed by immunoblotting with antibodies to APP (Fig. 5C and lower part of Fig. 5D) or to myc (upper part of Fig. 5D). The positions of the various proteins are indicated on the right of the immunoblots, and the locations of molecular weight standards are shown on the left.

10   Figs. 6A-F demonstrate the interaction of Fe65 with Tip60. Fig. 6A shows results of a quantitative yeast two-hybrid assay. Fig. 6B shows GST-pulldowns of myc-tagged Fe65 expressed in COS cells with wild-type and mutant GST-Tip60 proteins. Figs. 6C-F show immunofluorescence localization of tagged HA-Fe65 and myc-tagged Tip60 co-transfected into HeLa cells. Fig. 6C shows an

15   overview of two adjacent cells; Figs. 6D-F display individual and merged labeling patterns. Calibration bars = 10 μM.

Fig. 7A shows the results of transactivation of Gal4-Tip60 in COS cells co-transfected with full length or mutant Fe65 proteins and/or wild-type or mutant APP proteins. Fig. 7B shows the domain structure of Gal4-Tip60.

20   Fig. 8 provides a model for nuclear signaling mediated by the γ-cleavage product of APP in which APP is cleaved by α-, β- and γ-secretases, releasing the 47 residue cytoplasmic tail plus 10-12 hydrophobic residues from the TMR. The cytoplasmic tail complexed with Fe65 is translocated to the nucleus and interacts with Tip60 to regulate transcription.

DETAILED DESCRIPTION OF THE INVENTION

Proteolytic processing of APP produces, inter alia, amyloid-β peptide that contributes to the pathogenesis of Alzheimer's disease, and a C-terminal cytoplasmic tail of APP of unknown function until the present invention. In

5   accordance with the present invention, it has been discovered that the C-terminal cytoplasmic tail of APP engages in nuclear signaling. In particular, it has been discovered that the released cytoplasmic tail of APP forms a functional complex with the nuclear protein Fe65 and the histone acetyl-transferase Tip 60, and that the complex is a potent stimulator of transcription by heterologous DNA-binding

10   domains. This understanding of the role of the cytoplasmic tail of APP in nuclear signaling has led to the development of an assay to identify agents that affect the cleavage of APP. Such agents are useful as candidate therapeutics for the treatment of Alzheimer's disease, and as models for rational drug design.

In one embodiment, the present invention provides a method of

15   identifying an agent that affects the cleavage of APP comprising contacting a cell, wherein the cell contains APP modified in the C-terminal cytoplasmic tail to allow detection of nuclear localization, with a candidate agent and measuring nuclear localization of the C-terminal cytoplasmic cleavage product of APP in the presence and absence of a candidate agent. An agent that increases or decreases the nuclear

20   localization of the cleavage product relative to nuclear localization in the absence of the agent is defined as an agent that affects cleavage of APP.

The term APP as used herein includes naturally occurring mammalian APP and also APP that has been modified, for example in a way to facilitate measurement of nuclear localization of a cleavage product. Naturally occurring

25   human APP is a 695 amino acid protein, in which the C-terminal 47 residues are designated the cytoplasmic tail. The gene encoding APP, its splice variants, and resulting nucleotide and amino acid sequences are known in the art and disclosed for example by Kang et al. (1987) Nature 325, 733-736, Selkoe, supra; Bayer et al., supra; Haass et al., supra; and Price et al., supra, the disclosures of which are

30   incorporated herein by reference.

Further, APP as defined herein may include other modifications such as insertions, deletions and substitutions provided that the functions of ability of the cytoplasmic tail or part thereof to be cleaved from the remainder of APP and translocated to the nucleus are retained.

5   The C-terminal cytoplasmic tail of APP is modified allow detection of nuclear localization. The modification may be in any region of the cytoplasmic tail. The modification may be at the C-terminal or N-terminal end of the tail, for example at the junction of the transmembrane and cytoplasmic domains. In one embodiment, the cytoplasmic tail of APP is modified to include the DNA binding domain and the

10   activation domain of the same or different heterologous transcription factors. Heterologous as used herein means not derived from a gene encoding APP. In this embodiment, nuclear localization is measured by determining activation of transcription of an indicator gene that is under the transcriptional control of a binding site for the DNA binding domain. Transcription factors and their component DNA-

15   binding and activation domains are well-known in the art.

In a preferred embodiment, the cytoplasmic tail is modified to include a heterologous DNA-binding domain such as the DNA-binding domain of the yeast transcription factor Gal4, or the bacterial LexA DNA binding domain. The Gal4 and LexA DNA binding domains are known in the art and disclosed for example by

20   Giniger et al. (1985) Cell 40, 767-774 and Hurstel et al. (1986) EMBO J. 5, 793-798. The modification may further contain the transcriptional activation domain of Gal4, or another activator such as the viral VP16 activator, which is disclosed for example by Stringer et al. (1990) Nature 345, 783-786. In a preferred embodiment, the cytoplasmic tail of APP is modified to include Gal4 and VP16. A transcription factor

25   module of Gal4-VP16 is described by Sadowski et al. (1988) Nature 335, 563-564. In an alternative embodiment, a DNA-binding domain but not an activation domain is included with the cytoplasmic tail and the mammalian nuclear multidomain protein, Fe65, is added as a co-factor to facilitate transcriptional activation. Fe65 is known in the art and disclosed for example by Duilio et el. (1991) Nucleic Acids Res. 19, 5269-

30   5274. The term Fe65 as used herein includes modifications such as insertions, deletions and substitutions provided that the function of the ability of Fe65 to

facilitate transcriptional activation is maintained. For example, it has been demonstrated herein that the N-terminal third of Fe65 may be deleted without loss of this function.

Accordingly, the modification of the cytoplasmic tail may consist of a
5   heterologous DNA-binding domain, or a module consisting of a DNA-binding domain and a transcriptional activation domain, which may be from the same or different sources.

The indicator gene is operably linked to a binding site for the DNA-binding protein. For example, the indicator gene may be provided in the form
10   of a Gal4 or LexA dependent reporter plasmid containing an indicator gene such as luciferase or chloramphenicol acetyl transferase under the control of a Gal4 or LexA regulatory element, respectively, such as an upstream activating sequence. Translocation of the cytoplasmic tail of APP to the nucleus results in translocation of the transcription factor as well, resulting in activation of transcription of the marker
15   gene. Accordingly, detection of the marker gene product provides an assay for nuclear localization of the cytoplasmic tail of APP, and hence measures cleavage of APP. Transcriptional activation assays are described by Fields et al. (1989) Nature 340, 245-246, the disclosure of which is incorporated herein by reference. Gal4 and LexA reporter plasmids are described by Lillie et al. (1989) Nature (London) 338, 38-
20   44 and Hollenberg et al. (1995) Mol. Cell. Biol. 15:3813-3822.

Candidate agents that may be tested by the assays of the present invention include proteins, peptides, non-peptide small molecules, and any other source of therapeutic candidate agents. The agents may be naturally occurring or synthetic, and may be a single substance or a mixture. Screening may be performed
25   in high throughput format using combinatorial libraries, expression libraries and the like. Agents identified as affecting APP cleavage may be subsequently tested for biological activity and used as therapeutics or as models for rational drug design.

Cells useful for the assays of the present invention include eukaryotic cells in which the cytoplasmic tail cleavage product of APP can be translocated to the
30   nucleus. Suitable cells include, for example, insect and mammalian cells. Preferred cells include Schneider, PC12, COS, HeLa and HEK293 cells.

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Cells containing APP may be cells stably or transiently transfected with a construct encoding APP as described above using methods known to those of ordinary skill in the art. Constructs containing chimeric genes comprising a promoter operably linked to nucleic acid encoding APP and modified to include the DNA-

5   binding domain of a transcriptional activator, or a module comprising the DNA-binding domains and transcriptional activation domain of the same or different transcription factor, are constructed using well-known recombinant DNA methods. These constructs are co-transfected into cells with the corresponding reporter constructs described above. For cases in which the construct does not contain a

10   transcriptional activation domain, cells are also co-transfected with vector comprising a nucleic acid encoding Fe65 operably linked to a promoter. The promoter may be constitutive or inducible.

The transfected cells are contacted with an agent to be tested for its ability to affect APP cleavage. A detectable increase or decrease in nuclear

15   localization of the C-terminal cytoplasmic tail, as measured by a change in transcriptional activation of the indicator gene, is indicative of an agent that affects cleavage of APP. The cells may be contacted with the candidate agent before expression of modified APP is induced from an inducible promoter.

In a particularly preferred embodiment of the present invention human

20   APP is modified to include Gal4-VP16 within the cytoplasmic tail. In particular, Gal4-VP16 is inserted between residues 651 and 652 of APP. The modified APP is generated by means of a mammalian expression plasmid containing a chimeric gene encoding residues 1-651 of APP, Gal4, VP16, and residues 652-695 of APP (i.e. the cytoplasmic tail, APP ct) under the control of a promoter. The plasmid may further

25   comprise regulatory sequences, linkers, and other elements to facilitate cloning, replication, transfection and expression. A cell comprising the modified APP is provided by transfecting a cell, preferably a mammalian cell, and most preferably a human cell, with the expression plasmid. The cell is cotransfected with a Gal4 reporter plasmid in which luciferase mRNA is driven by multiple copies of the Gal4

30   upstream activating sequence (UAS). When the modified APP is cleaved by γ-secretase, the cleavage product containing Gal4-VP16 enters the nucleus and

transactivates transcription from the Gal4 reporter plasmid. Expression of luciferase is measured by standard assays, for example by measuring luciferase activity using a commercially available kit. Luciferase expression is a measure of transactivation, which is in turn a measure of APP cleavage.

5   The transfected cells are contacted with a candidate agent, and luciferase expression is measured in the presence and absence of the agent. An agent that increases or decreases luciferase expression is an agent that affects APP cleavage.

In another embodiment, the present invention provides a method of identifying an agent that affects the cleavage of APP comprising providing a cell,

10   wherein the cell contains APP and a protein that interacts with the C-terminal cleavage product of APP in the nucleus to activate transcription, and wherein the protein is modified to allow detection of nuclear translocation of the C-terminal cytoplasmic cleavage product; contacting the cell with a candidate agent; and measuring nuclear localization of the C-terminal cytoplasmic cleavage product in the

15   presence and absence of the agent. An agent that increases or decreases nuclear localization of the C-terminal cleavage product relative to nuclear localization in the absence of the cleavage product is defined as an agent that affects cleavage of APP.

In accordance with the present invention, it has been discovered that the C-terminal cytoplasmic cleavage product of APP may interact with one or more

20   other proteins to activate transcription. Accordingly, cleavage of APP can be detected by modifying a protein that interacts, directly or indirectly, with the cleavage product. Direct interaction refers to proteins that form a complex with the cleavage product. Indirect action includes proteins that interact with other proteins that are targets of the cleavage product, and thereby includes, for example, proteins that interact with Fe65

25   and/or Tip60 in the regulation of transcription. A preferred protein is the histone acetyl-transferase Tip60. In a preferred embodiment of this method, a protein that interacts with the C-terminal cleavage product of APP to activate transcription, for example Tip60 is modified to allow detection of nuclear localization, for example by fusion with the DNA binding domain of a transcriptional activator such as Gal4 or

30   LexA. Nuclear localization is measured by determining activation of transcription of

an indicator gene that is under the transcriptional control of a binding site for the DNA binding domain, as described hereinabove.

The nucleotide and amino acid sequences of Tip60 are known in the art and disclosed for example by Kamine et al. (1996) Virology 216, 357-366 and Ran et al. (2000) Gene 258, 141-146. The term Tip60 as used herein includes modifications such as insertions, deletions and substitutions provided that the ability of Tip60 to interact with the C-terminal cytoplasmic cleavage product of APP is maintained.

In a preferred embodiment of this method, the cells contain APP, Fe65 and Tip60 modified to contain the DNA binding domain of a transcriptional activator, preferably Gal4. Such cells may be obtained by co-transfection with plasmids containing nucleic acids encoding APP, Fe65, and modified Tip60. Plasmids may further comprise regulatory sequences, linkers and other elements to facilitate cloning, replication, transfection and expression. Cells are eukaryotic, including for example insect and mammalian, and preferably human. Cells are also co-transfected with the appropriate reporter plasmid as described above. Expression of the reporter gene is a measure of transactivation, which is in turn a measure of nuclear localization of the C-terminal cytoplasmic cleavage product of APP, and thus APP cleavage. Reporter gene expression is measured as described hereinabove.

In another embodiment the present invention provides vectors that contain nucleic acids encoding the modified APP. In a preferred embodiment, the vector comprises a nucleic acid encoding APP operably linked to a promoter wherein a nucleic acid module encoding a heterologous DNA binding domain of a transcription factor and a transcriptional activator of the same or a different transcription factor is contained within the portion of the nucleic acid that encodes the C-terminal cytoplasmic tail of APP. A module "within" the tail includes embodiments in which the module is at the 5'-end or 3'-end of the region encoding the cytoplasmic tail. In a preferred embodiment the module is Gal4-VP16. The vectors may further comprise regulatory sequences, linkers, and other elements to facilitate cloning, replication, transfection and expression.

The present invention further provides vectors that comprise a nucleic acid encoding APP operably linked to a promoter wherein a nucleic acid encoding a heterologous DNA binding domain of a transcription factor is contained with the portion of the nucleic acid that encodes the C-terminal cytoplasmic tail of APP. The

5   DNA binding domain may be at the 5'-end or 3'-end of the region encoding the cytoplasmic tail. In a preferred embodiment the DNA binding domain is Gal4. The vectors may further comprise regulatory sequences, linkers, and other elements to facilitate cloning, replication, transfection and expression.

The present invention further provides vectors that comprise a nucleic

10   acid encoding Tip60 and the DNA binding domain of a transcription factor wherein the nucleic acid is operably linked to a promoter. In a preferred embodiment the DNA binding domain is Gal4.. The vectors may further comprise regulatory sequences, linkers, and other elements to facilitate cloning, replication, transfection and expression.

15   The present invention further provides cells containing the foregoing vectors. The cells are eukaryotic, preferably mammalian, and most preferably human. Cells containing the vectors of the invention may be obtained by methods known in the art, and may be transiently or stably transfected. The cells may also further contain a corresponding reporter plasmid as described hereinabove.

20   In another embodiment, the present invention provides agents that affect cleavage of APP identified by the method of the present invention. Compositions comprising the agents are also provided. The compositions may comprise carriers and/or diluents such as solvents, dispersion media, antibacterial and antifungal agents, microcapsules, liposomes, cationic lipid carriers, isotonic and

25   absorption delaying agents and the like, as well as supplementary active ingredients.

The present invention further provides kits useful for identifying an agent that affects cleavage of APP. The kits comprise a first compartment containing cells comprising a vector that encodes a modified APP of the invention. The cells may further contain a reporter plasmid. The kits may further comprise a second

30   compartment containing a means for measuring expression of an indicator gene contained in the reporter plasmid.

In another embodiment, the kits comprise a first compartment containing a vector that encodes a modified APP of the invention. The kits may further comprise a second compartment containing a reporter plasmid, and may further comprise a third compartment containing cells suitable for transfection by the

5   vector of the first compartment.

In a further embodiment, the kits comprise a first compartment containing a vector comprising a nucleic acid encoding APP operably linked to a promoter, a second compartment containing a vector comprising a nucleic acid encoding Fe65 operably linked to a promoter, and a third compartment containing a

10   nucleic acid encoding a fusion protein comprising Tip60 and the DNA binding domain of a transcriptional activator, preferably Gal4.

The following nonlimiting examples serve to further illustrate the present invention.

Example I

15   ### Materials and Methods

The following materials and methods were used in subsequent examples.

1. Transactivation assays

1.1 General design

20   PC12, COS, HeLa, and HEK293 cells were co-transfected at 50-80% confluency in 6-well plates using Fugene6 (Roche, Indianapolis, IN), and 3-4 plasmids (0.1-1.0 µg DNA/well depending on cell types; see plasmid list below for description of all constructs). All transfections included a. Gal4 (pG5E1B-luc) or LexA (pL8G5-luc) reporter plasmids; b. constitutively expressed ß-galactosidase

25   expression plasmid (pCMV-LacZ) to control for transfection efficiency; and c. the Gal4- or LexA-fusion protein vectors. Cells were harvested 48 hr post-transfection in 0.2 ml/well reporter lysis buffer (Promega, Madison, WI), and their luciferase and ß-galactosidase activities were determined with the Promega luciferase assay kit and the standard O-nitrophenyl -D-galacto-pyranoside method, respectively. The luciferase

30   activity was standardized by the ß-galactosidase activity to control for transfection efficiency and general effects on transcription, and in most experiments further

normalized for the transactivation observed in cells expressing Gal4 or LexA alone. Values shown are averages of transactivation assays carried out in duplicate, and repeated at least three times for each cell type and constructs. Most constructs were assayed in three or four cell lines, but usually only representative results for one cell

5   line are shown. To confirm expression of transfected proteins and secretase cleavage of the various APP constructs, transfected cells were also analyzed by immunoblotting using antibodies to the respective proteins and/or antibodies to the epitope tags attached to the proteins.

1.2 Amounts of DNA used

10   *1.2.1. APP-Gal4VP16 assays*

Plasmids used in the following amounts: a. pG5E1B-luc (HEK293 cells, HeLa cells, and COS cells = 0.3-0.5 μg DNA; PC12 cells = 1.0 μg); b. pCMV-LacZ (HEK293 cells, HeLa cells, and COS cells = 0.05 μg DNA; PC12 cells = 0.5 μg DNA); c. pMst (Gal4), pMst-GV-APP (APP-GV), pMst-GV (GV), pMst-GV-APPct

15   (APPct-GV), pMst-APPct (APPct-Gal4), pMst-GV-APP* (APP*-GV), pMst-GV-APPγ* (APPγ*-GV), pMst-APPct* (APPct*-Gal4), pMst-GV-APPα (APPα-GV), pMst-GV-NRX (NRX-GV), pMst-GV-NA (NRXe-GV-APPc), pMst-GV-AN (APPe-GV-NRXc)(HEK293, HeLa, and COS cells = 0.1-0.3 μg DNA; PC12 cells = 1.0 μg DNA). d. pcDNA3.1-PS2D366A, pCMV-Mint1, or pCMV5-Fe65 (HEK293, HeLa,

20   and COS cells = 0.1-0.3 μg DNA; PC12 cells = 0.5 μg DNA).

1.2.2. APP-Gal4 and APP-LexA assays with and without various Fe65 and Mint1 constructs

For transactivation by APP-Gal4 and APP-LexA constructs, cells were cotransfected with: a. pG5E1B-luc (Gal4 reporter plasmid) or pL8G5-luc (LexA-

25   reporter plasmid) (HEK293 cells, HeLa cells, and COS cells = 0.3 μg DNA; PC12 cells = 1.0 μg); b. pCMV-LacZ (ß-galactosidase control plasmid. HEK293 cells, HeLa cells, and COS cells = 0.05 μg DNA; PC12 cells = 0.2-0.5 μg DNA); c. pMst (Gal4), pMst-APP (APP-Gal4), pMst-APP* (APP*-Gal4), pMst-APPγ (APPγ-Gal4), pMst-APPγ* (APPγ*-Gal4), pMst-AN-APPc32 (APP-G-NRX-APPc32), pMst-AN

30   (APPe-G-NRXc), pML (LexA), pML-APP (APP-LexA), pML-APP* (APP*-LexA),

pML-APPct (APPct-LexA), pML-APPct* (APPct*-LexA) (HEK293 cells, HeLa cells, and COS cells = 0.3-0.5 µg DNA; PC12 cells = 1.0-1.5 µg); and d. pCMV-Mint1 (mint1) or pCMV5-Fe65 (Fe65) (HEK293 cells, HeLa cells, and COS cells = 0.3-0.5 µg DNA; PC12 cells = 1.0-1.5 µg) where indicated.

5   For transactivation assays of Fe65 mutants, cells were cotransfected with: a. pG5E1B-luc (Gal4 reporter plasmid) or pL8G5-luc (LexA-reporter plasmid); b. pCMV-LacZ (ß-galactosidase control plasmid); c. pMst (Gal4), pMst-APP (APP-Gal4), pML (LexA), or pML-APP (APP-LexA); and d. pCMV5-Fe65 (Fe65), pCMVMyc-Fe65(128-711) (Fe65(128-711)), pCMVMyc-Fe65(242-711) (Fe65(242-

10   711)), pCMVMyc-Fe65(287-711) (Fe65(287-711)), pCMV5-Fe65(1-553) (Fe65ΔPTB2), pCMVMyc-Fe65ΔPTB1 (Fe65ΔPTB1), pCMV5-Fe65mW1(Fe65mW1), pCMV5-Fe65mW2 (Fe65mW2), pCMV5-Fe65mW3 (Fe65mW3), pCMV5-Fe65mW4 (Fe65mW4), or pCMV5-Fe65mW5 (Fe65mW5) where indicated. a. and b.: amounts of DNA same as under 1.21. c. and d.:0.3-0.5 µg

15   DNA for COS, HeLa, and HEK293 cells; 1.0-1.5 µg DNA for PC12 cells.

1.2.3. Gal4-Tip60 assays

        For transactivation assays of Gal4-Tip60, COS and HEK293 cells were cotransfected with: a. pG5E1B-luc (Gal4 reporter plasmid, 0.3 µg DNA); b. pCMV-LacZ (ß-galactosidase control plasmid, 0.05 µg DNA); c. pMst (Gal4); pM-Tip60 (rat

20   Gal4-Tip60 β residues 63-454); pM-Tip60* (mutant rat Gal4-Tip60 β residues 63-454); pM-hTip60 (full-length wild type human Gal4-Tip60 β); or pM-hTip60* (full-length mutant human Gal4-Tip60 β) (0.4 µg DNA) d. pCMV5-Fe65 (Fe65), pCMVMyc-Fe65(242-711) (Fe65(242-711)), pCMV5-Fe65(1-553) (Fe65ΔPTB2), or pCMV5-Fe65mW4 (Fe65mW4) (0.3 µg DNA) where indicated; and e. pCMV5-APP

25   (human APP695) or pCMV5-APP* (mutant human APP695) (0.3 µg DNA). All transfections contained one of the plasmids listed in a-c, whereas d and e were variable.

2. <u>Yeast Two-hybrid screens for APP- and Fe65-binding proteins</u>

2.1 APP screens

- **Bait:** <u>pBTM116-APP</u>
- **Yeast strain:** L40
5
- **Library:** P8 rat brain library constructed in prey vector pVP16-3.
- **Screening condition:** 250 ml mid-log phase yeasts harboring the bait vector pBTM116-APP were transformed with 125 µg of P8 rat brain library plasmids, and plated on CSM-Trp-Leu-His plates supplemented with 5 mM 3-amino-1,2,4-triazole. 2×10^7 total transformants were obtained. Around 250 positives appeared
10   after 3 days incubation at 30°C. 80 positives were recovered and identified by sequencing or Southern blotting. Among them, 72 are Fe65 and one is Fe65-like protein 2 (Fe65LP2).
- **Summary of Fe65 prey clones that were sequenced**

Prey Clones	Insert Size (kb)	Residues	Extra Residues
P29[a]	3.1	1-711	43
P50, P64, P65, P69	2.9	1-711	43
P42	3.0	48-711	0
P60[a]	2.6	128-711	0
P6[a], P7, P18	1.9	242-711	8
P57	2.3	242-711	50
P19, P25[b]	1.0	242-?	21
P15, P27[a]	1.6	287-711	0
P21	1.5	301-711	0
P4, P22	1.4	313-711	0
P9, P16, P17	1.9	321-711	0
P39	1.4	339-711	0

[a]P29, P60, P6, P27 were used to generate pCMV5-Fe65, pCMVMyc-Fe65(128-711),
15   pCMVMycFe65(242-711), and pCMVMyc-Fe65(287-711), respectively.

[b]P25 insert (1.0kb) was used as Southern blotting probe to identify the rest of the recovered prey clones.

2.2 Fe65 screens

- **Bait:** <u>pLexN-Fe65(287-711)</u>
20
- **Yeast strain:** L40
- **Library:** P8 rat brain library constructed in prey vector pVP16-3.

- **Screening condition:** 250 ml mid-log phase yeasts harboring the bait vector pLexN-Fe65(287-711) were transformed with 125 µg of P8 rat brain library plasmids, and plated on CSM-Trp-Leu-His plates supplemented with 25 mM 3-amino-1,2,4-triazole. 7×10^7 total transformants were obtained, and ~300 positives

5   selected after 3 days incubation at 30 °C.

Summary of prey clones that were sequenced: Tip60 ß (residues 63-454) = 8 clones; APLP1 = 9 clones.

3. Quantitative yeast two-hybrid assays

For quantitative measurements of yeast two-hybrid interactions,

10   various bait and prey plasmids were co-transfected into yeast strain L40 and plated on CSM-Trp-Leu (Bio101) plates. Single colonies from the CSM-Trp-Leu plates were cultured in CSM-Trp-Leu liquid medium after 3 days, and re-inoculated into YPAD medium at $OD_{600}=0.3$ on the following day. When the yeast cultures reached mid-log phase ($OD_{600}=0.6-1.0$), cells were collected by centrifugation, washed in Z buffer

15   (16.1 g/l $Na_2HPO_4 \cdot 7H_2O$, 5.5 g/l $NaH_2PO_4 \cdot H_2O$, 0.75 g/l KCl, 0.246 g/l $MgSO_4 \cdot 7H_2O$ pH 7.0), and resuspended in 100 µl Z buffer. Cells were lysed by three freeze-thawing cycles, 0.8 ml reaction solution (0.5 g/l ONPG and 0.024% ß-mercaptoethanol in Z buffer) was added, and reactions were stopped with 0.4 ml 1M Na_2CO_3 at the appropriate time points depending on color development. After centrifugation (14,000

20   x g for 10 min), OD_{420} was measured, and the relative ß-galactosidase activity was calculated as 1000 x OD_{420}/(min x vol. yeast in ml x OD_{600}).

3.1   APP & Fe65

#	Bait	Prey	OD_{600}	Time(min)	OD_{420}	β-gal unit	Mean	S.D.
1	APPct	P29(Fe65 1-711)	0.899	15	5.025	372.6363	423.8138	48.30529
			0.764	15	4.93	430.192		
			0.685	15	4.815	468.6131		
2	APPct	Fe65mW5	0.657	15	4.895	496.7022	449.4991	71.701238
			0.68	15	4.945	484.8039		
			0.822	15	4.525	366.9911		
3	APPct	Vector	0.813	15	0.004	0.328003	0.370065	0.0425321
			0.903	15	0.005	0.36914		
			0.807	15	0.005	0.413052		
4	APPct*	P29(Fe65 1-711)	0.776	15	0.005	0.429553	0.506697	0.0674611
			0.601	15	0.005	0.554631		
			0.622	15	0.005	0.535906		
5	APPct*	Fe65mW5	0.631	15	0.004	0.42261	0.44523	0.0467628
			0.644	15	0.004	0.414079		
			0.668	15	0.005	0.499002		

a. APPct and P29(Fe65 1-711) are bait and prey clones described in the section on the Yeast two-hybrid screen for APP-binding proteins.

b. APPct* was expressed from pBTM116-APP*, which was generated by QuickChange site-directed mutagenesis kit (Stratagene, LaJolla, CA) to mutate *684NPTY* to *684NATA* with pBTM116-APP as the template.

c. Fe65mW5 was expressed from pVP16-3-Fe65mW5, which encodes full-length rat Fe65 (1-711 residues) with *Y270A, Y271A, W272A, W281F,* and *P284A* mutations.

3.2   Fe65 & LBP-1c

#	Bait	Prey	OD_{600}	Time(min)	OD_{420}	β-gal unit	Mean	S.D.
1	Fe65(287-711)	LBP-1c	0.747	60	0.037	0.825524	0.772376	0.1010779
			0.737	60	0.029	0.655812		
			0.678	60	0.034	0.835792		
2	Fe65(287-531)	LBP-1c	0.686	60	0.167	4.057337	4.438847	0.3744772
			0.704	60	0.203	4.805871		
			0.625	60	0.167	4.453333		
3	Fe65(287-711)	vector	0.709	60	0.006	0.141044	0.15965	0.0262405
			0.703	60	0.008	0.189663		
			0.787	60	0.007	0.148242		
4	Fe65(287-531)	vector	0.725	60	0.022	0.505747	0.5543	0.0714302
			0.681	60	0.026	0.636319		
			0.672	60	0.021	0.520833		
5	Lamin	LBP-1c	0.626	60	0.017	0.452609	0.721477	0.3382954
			0.819	60	0.03	0.610501		
			0.454	60	0.03	1.101322		

a. Fe65(287-711) and Fe65(287-531) were expressed from pLexN-Fe65(287-711) and

pLexN-Fe65(287-531), respectively. Lamin was expressed from pBTM116-Lamin.

b. LBP-1c was expressed from pVP16-3-LBP-1c, which encodes full-length human

5   LBP-1c (1-450 residues). References: Z. Bing, S.A.G. Reddy, Y. Ren, J.Qin, and

W.S.L. Liao (1999) J. Biol. Chem. 274, 24649-24656. N. Zambrano, G. Minopoli, P.

de Candia, and T. Russo (1998) J. Biol. Chem. 273, 20128-20133.

3.3   Fe65 & hTip60

#	Bait	Prey	OD_{600}	Time(min)	OD_{420}	β-gal unit	Mean	S.D.
1	Fe65(287-711)	hTip60	0.806	15	4.905	405.7072	431.7927	45.395309
			0.818	15	4.975	405.4605		
			0.665	15	4.83	484.2105		
2	Fe65(287-531)	hTip60	0.695	15	3.895	373.6211	391.1748	52.914479
			0.774	15	4.055	349.2679		
			0.682	15	4.61	450.6354		
3	Fe65(287-711)	vector	0.709	60	0.006	0.141044	0.15965	0.0262405
			0.703	60	0.008	0.189663		
			0.787	60	0.007	0.148242		
4	Fe65(287-531)	vector	0.725	60	0.022	0.505747	0.5543	0.0714302
			0.681	60	0.026	0.636319		
			0.672	60	0.021	0.520833		
5	Lamin	hTip60	0.594	15	0.011	1.234568	1.751572	0.5012274
			0.635	15	0.017	1.784777		
			0.507	15	0.017	2.235371		

a. Fe65(287-711) and Fe65(287-531) were expressed from pLexN-Fe65(287-711) and
pLexN-Fe65(287-531), respectively. Lamin was expressed from pBTM116-Lamin.

b. hTip60 was expressed from pVP16-3-hTip60 which encodes full-length human
Tip60β (residues 1-461). Reference: Qitao Ran and Olivia M. Pereira-Smith (2000)
5   Gene 258, 141-146.

4. Plasmid list

4.1 Standard plasmids

pCMV-LacZ: Transfection control plasmid encoding bacterial
ß-galactosidase under control of the CMV promoter.

10   pG5E1B-luc: Gal4 reporter plasmid (Lillie, J. W., and M. R. Green.
1989. Transcription activation by the adenovirus E1a protein. Nature (London)
338:39-44) in which luciferase mRNA is driven by five copies of Gal4 UAS.

pL8G5-luc: LexA reporter plasmid in which luciferase mRNA is
driven by eight copies of the LexA binding site and five copies of Gal UAS.

15   (Hollenberg, S. M., Sternglanz, R., Cheng, P. F., and Weintraub H. 1995.
Identification of a new family of tissue-specific basic Helix-Loop-Helix proteins with
a two-hybrid system. Mol. Cell. Biol. 15:3813-3822).

pMst: Gal4 expression vector driven by the SV40 promoter derived from pM (Clontech, Palo Alto, CA) by mutating the stop codon before the Gal4 DNA-binding domain.

pMst-GV: Gal4 VP16 (GV) expression vector generated by cloning the

5   VP16 activation domain (residues 413-490) into the EcoRI/BamHI sites of pMst (linker sequence between Gal4 and VP16: QLTVS*PEF*APPTD).

pML: LexA expression vector generated by replacing the NheI/EcoRI fragment of pM (Clontech) with the PCR amplified LexA-coding sequence.

4.2 APP plasmids

10   *4.2.1. Mammalian expression plasmids*

pMst-GV-APPct, encodes APPct-GV generated by cloning the cytoplasmic tail of human APP695 (APPct, residues 652-695) into the BamHI/SalI sites of pMst-GV (linker sequence between GV and APPct = DEYGG*GIPPG*QYTSI).

15   pMst-GV-APPct*, encodes APPct*-GV with point mutations in the cytoplasmic tail of APP (residues 684-687; wild type sequence = NPTY; mutant sequence = NATA). Generated by QuickChange site-directed mutagenesis (Stratagene) with pMst-GV-APPct as template.

pMst-GV-APP encodes APP-GV. Generated by cloning a PCR

20   fragment encoding residues 1-651 of human APP695 into the NheI site of pMst-GV-APPct (linker sequence between APPe and GV = MLKKK*PLASSR*MKLLS).

pMst-GV-APP*, encodes APP*-GV with point mutations in the cytoplasmic tail of APP (residues 684-687; wild type sequence = NPTY; mutant sequence = NATA). Generated by QuickChange site-directed mutagenesis

25   (Stratagene) with pMst-GV-APP as the template.

pMst-GV-APPγ, encodes APPγ-GV containing an N-terminal methionine followed by residues 639-651 of human APP695, Gal4-VP16, and residues 652-695 of APP695. Obtained by inserting the PCR-amplified residues 639-651 into the BglII/NheI sites of pMst-GV-APPct (linker sequence between TMR of

30   APP and Gal4 = MLKKK*PLASSR*MKLLS).

pMst-GV-APPγ*, encodes APPγ*-GV corresponding to APPγ-GV with the mutation in the NPTY sequence. Generated by QuickChange site-directed mutagenesis (Stratagene) with pMst-GV-APPγ as the template.

pMst-APPct, encodes APPct-Gal4. Generated by cloning the cytoplasmic tail of human APP695 (APPct, residues 652-695) into the BamHI/SalI sites of pMst (linker sequence between Gal4 and APPct = QLTVS*PEFPGIPPG*QYTSI).

pMst-APPct*, encodes APPct*-Gal4 corresponding to APPct-Gal4 with the NPTY mutation. Generated by cloning the mutant cytoplasmic tail from pMst-GV-APPct* into the BamHI/SalI sites of pMst.

pMst-APP, encodes APP-Gal4. Generated by cloning a PCR fragment containing the extracellular and transmembrane region of human APP695 (APPe, residues 1-651) into the NheI site of pMst-APPct (linker sequence between APPe and Gal4 = MLKKK*PLASSR*MKLLS).

pMst-APP*, encodes APP*-Gal4. Obtained as pMst-APP, but cloned into the NheI site of pMst-APPct*.

pMst-APPγ, encodes APPγ-Gal4. Generated by cloning a PCR fragment coding for a methionine and residues 639-651 of human APP695 into the BglII/NheI sites of pMst-APPct (linker sequence between TMR and Gal4 =MLKKK*PLASSR*MKLLS).

pMst-APPγ*, encodes APPγ*-Gal4. Obtained as pMst-APPγ, but cloned into pMst-APPct*.

pMst-GV-NRX, encodes NRX-GV. Generated by sequential cloning of PCR fragments coding for the cytoplasmic tail of rat neurexin I (βNRXct, residues 414-468) and the extracellular and transmembrane regions (NRXe, residues 1-417) into the BamHI/SalI and the NheI sites, respectively, of pMst-GV (linker sequences between NRXe and Gal4 = MYKYR*TLASSR*MKLLS; between VP16 and NRXct = DEYGG*GIPPG*YKYRN).

pMst-GV-NA, , encodes NRXe-GV-APPc. Generated by cloning a PCR fragment corresponding to NRXe into the NheI site of pMst-GV-APPct (linker sequence between NRXe and Gal4 = MYKYR*TLASSR*MKLLS).

<u>pMst-GV-AN</u>, encodes APPe-GV-NRXc. Generated by sequential cloning of PCR fragments corresponding to NRXc and APPe into the BamHI/SalI and the NheI sites, respectively, of pMst-GV (linker sequences between APPe and Gal4 = MLKKK*PLASSR*MKLLS; between VP16 and NRXct = DEYGG*GIPPG*YKYRN).

5.   <u>pMst-AN</u> encodes APPe-G-NRXc. Generated as pMst-GV-AN, but into pMst (linker sequences between APPe and Gal4 = MLKKK*PLASSR*MKLLS, and between Gal4 and NRXct = QLTVS*PEFPGIPPG*YKYRN.

<u>pMst-AN-APPc32</u>, encodes APP-G-NRX-APPc32. Generated from pMst-AN by inserting a PCR fragment encoding the C-terminal 32 residues of human

10   APP695 (APPc32) into the rat neurexin I cytoplasmic tail (NRXct) between residue 425 and 427, with V426 deleted during the cloning (linker sequences between APPc32 and NRXct = EGSYH*IDD*AAVT, and between APPc32 and NRXct = EQMQN*I*DESRN.

<u>pML-APPct</u>, encodes APPct-LexA. Generated by replacing the Gal4

15   sequence (the NheI/EcoRI fragment) in pMst-APPct with the LexA-sequence (linker sequence between LexA and APPct = NGDWL*EFPGIPPG*QYTSI).

<u>pML-APPct*</u>, encodes APPct*-LexA. Generated as pML-APPct in pMst-APPct*.

<u>pML-APP</u>, encodes APP-LexA. Generated by cloning the

20   extracellular and transmembrane region of human APP695 (APPe, residues 1-651) into the NheI site of pML-APPct (linker sequence between APPe and LexA = MLKKK*PLAK*MKALT).

<u>pML-APP*</u>, encodes APP*-LexA. Generated as pML-APP with pML-APPct*.

25   <u>pCMV5-APP</u>, encodes full-length human APP695 inserted into the blunted-EcoRI/XbaI sites of pCMV5.

<u>pCMV5-APP*</u>, encodes full length human APP695 containing point mutations in the cytoplasmic NPTY sequence. Generated by QuickChange site-directed mutagenesis (Stratagene) with pCMV5-APP.

4.2.2. Yeast two-hybrid plasmids

pBTM116-APP, encodes residues 648-695 of human APP695 cloned into the BamHI/SalI sites of the yeast two-hybrid bait vector pBTM116 using a PCR fragment.

5   pBTM116-APP* = pBTM116-APP in which the codons encoding the NPTY sequence in the APP cytoplasmic tail were mutated to NATA using QuickChange site-directed mutagenesis (Stratagene).

4.3 Fe65 plasmids

4.3.1. Mammalian expression plasmids

10   pCMV5-Fe65: encodes full-length rat Fe65 (711 residues). Constructed by sub-cloning the 3 kb SalI fragment from the yeast two-hybrid prey clone #P29 into the SalI site of pCMV5.

pCMVMyc-Fe65(128-711): encodes residues 128-711 of Fe65. Generated by cloning the blunt-ended ..... fragment from the rat Fe65 cDNA into the

15   blunted EcoRI site in pCMVMyc.

pCMVMyc-Fe65(242-711): encodes residues 242-711 of Fe65. Generated by cloning the blunt-ended ..... fragment from the rat Fe65 cDNA into the blunted EcoRI site in pCMVMyc.

pCMVMyc-Fe65(287-711): encodes residues 287-711 of Fe65.

20   Generated by cloning the blunt-ended ..... fragment from the rat Fe65 cDNA into the blunted EcoRI site in pCMVMyc.

pCMV5-Fe65(1-553): encodes Fe65 PTB2 which lacks residues 554-711 of Fe65. Generated by introducing a stop codon into pCMV5-Fe65 after residue 553 with the QuickChange site directed mutagenesis kit (Stratagene).

25   pCMVMyc-Fe65 ΔPTB1: encodes Fe65 ΔPTB1 which lacks residues 314-440. Generated by sequentially cloning the PCR fragments encoding residues 441-711 and residues 1-313 of rat Fe65 into the ClaI and MluI sites, respectively, of pCMVMyc.

pCMV5-Fe65mW1: encodes Fe65mW1 point mutant in carrying

30   substitutions $W281F$ and $P284A$. Generated by QuickChange site directed mutagenesis (Stratagene) with pCMV5-Fe65 as template.

pCMV5-Fe65mW2: encodes Fe65mW2 point mutant in carrying substitution *W260F*. Generated by QuickChange site directed mutagenesis (Stratagene) with pCMV5-Fe65 as template.

pCMV5-Fe65mW3: encodes Fe65mW3 point mutant in carrying
5   substitutions *W260F*, *W281F* and *P284A*. Generated by QuickChange site directed mutagenesis (Stratagene) with pCMV5-Fe65mW1 as template.

pCMV5-Fe65mW4: encodes Fe65mW4 point mutant in carrying substitutions *Y270A*, *Y271A*, and *W272A*. The insert (2.1kb) can be cut out by HindIII+SalI double digestion.

10   pCMV5-Fe65mW5: encodes Fe65mW4 point mutant in carrying substitutions *Y270A*, *Y271A*, *W272A*, *W281F*, and *P284A*. The insert (2.1kb) can be cut out by HindIII+SalI double digestion.

pcDNA3.1-N-HA-Fe65: encodes full-length rat Fe65 preceded by a hemagglutinin (HA) epitope. Obtained by subcloning the rat Fe65 cDNA into the
15   blunted-EcoRI/XbaI sites of pcDNA3.1-N-HA.

4.3.2. Yeast two-hybrid plasmids

pLexN-Fe65(287-711), encodes residues 287-711 of Fe65 in the SalI/blunted-PstI sites in pLexN.

pLexN-Fe65(287-531), encodes residues 287-531 of Fe65 in the
20   BamHI/blunted-SalI sites in pLexN. Insert (740 bp) can be cut out by BamHI+PstI double digestion.

pVP16-3-Fe65mW5, encodes the mW5 mutant of Fe65 (see pCMV vectors above). Was generated by cloning the blunted 2.1 kb HindIII/XbaI fragment from pCMV5-Fe65mW5 into the blunted-NotI/XbaI sites of the yeast prey vector
25   pVP16-3. The insert can be cut out by SalI.

4.4 Tip60 plasmids

4.4.1. pCMV expression plasmids

pCMVMyc-Tip60(63-454), encodes residues 63-454 of rat Tip60β.
Generated by cloning the 1.3 kb EcoRI fragment from yeast two-hybrid prey clone
30   #B36 into the EcoRI site of pCMVMyc.

pCMVMyc-Tip60(63-454)*, encodes residues 63-454 of rat Tip60β with a mutation in residues 257-260 (sequences: wildtype = NKSY; mutant = NASA). Generated by QuickChange site directed mutagenesis kit (Stratagene) with · pCMVMyc-Tip60(63-454) as template.

5   pM-Tip60 encodes rat Tip60β residues 63-454 preceded by the Gal4 DNA-binding domain. Generated by subcloning the 1.3 kb BamHI/XbaI fragment from prey clone #36 into the BamHI/XbaI sites of pM.

pM-Tip60* encodes the same protein as pM-Tip60 with the inactivating mutation in residues 257-260. Generated by cloning the 1.3 kb

10   BamHI/XbaI fragment from pVP16-3-Tip60* into the BamHI/XbaI sites of pM.

pCMVMyc-hTip60 encodes myc-tagged full-length human Tip60ß. Obtained by subcloning the insert of EST IMAGE clone 2901054 into the MluI/XbaI sites of pCMVMyc.

pM-hTip60 encodes full-length human Tip60β preceded by the Gal4-

15   DNA binding domain. Obtained by cloning the blunted 1.6 kb EcoRI/NotI fragment from EST clone 2901054 into the blunted EcoRI site of pM. Insert can be cut out by SalI.

pM-hTip60*, same as pM-hTip60 but with the inactivating mutation in residues 257-260. Generated by QuickChange site directed mutagenesis (Stratagene)

20   with pM-hTip60 as template.

4.5 Yeast two-hybrid plasmids

Prey clone #B36 in pVP16-3; identified in yeast two-hybrid screens with pLexN-Fe65(287-711) as the bait in a P8 rat brain library. B36 encodes rat Tip60ß corresponding to residues 63-454 of human Tip60, with a single amino acid

25   change between human and rat sequences.

pVP16-3-Tip60* encoding mutant rat Tip60 with the inactivating mutation in residues 257-260 (sequences: wildtype = NKSY; mutant = NASA).Generated by cloning the EcoRI fragment from pCMVMyc-Tip60(63-454)* into the EcoRI site of yeast prey vector pVP16-3.

30   pVP16-3-hTip60, full-length human Tip60 cloned into the EcoRI/NotI sites of pVP16-3.

4.6 GST-fusion protein plasmids

pGEX-KG-Tip60(63-454), residues 63-454 Tip60ß fused to GST. Generated by cloning the 1.3 kb EcoRI fragment (1.3kb) of the yeast two-hybrid prey clone B36 into the EcoRI site of pGEX-KG.

5   pGEX-KG-Tip60(63-454)*, encodes residues 63-454 Tip60ß fused to GST. Generated as pGEX-KG-Tip60(63-454), but from pVP16-3-Tip60(63-454)*.

5. Miscellaneous plasmids

5.1 pCMV expression plasmids

pCMV5-Mint-1: rat Mint1 cloned into the EcoRI site of pCMV5

10   (Okamoto, M. and Südhof, T.C. (1997) *J. Biol. Chem.* 272, 31459-31464.)

pCS2+MT-SEF: Myc-tagged full-length human LBP-1c (1-450 residues) was expressed from control of the CMV promoter (gift from Dr. W.S.L. Liao, University of Texas MD Anderson Cancer Center, Houston TX; reference: Z. Bing, S.A.G. Reddy, Y. Ren, J. Qin, and W.S.L. Liao (1999) *J. Biol. Chem.* 274,

15   24649-24656.)

pcDNA3.1-PS2D366A (kind gift of Dr. C. Haass, Munich): encodes a dominant negative mutant of human presenilin 2 in pcDNA3.1.

5.2 Yeast two-hybrid plasmids

pVP16-3-LBP-1c, encodes full-length human LBP-1c. Generated by

20   cloning the blunted 1.4 kb XhoI fragment from pCS2+MT-SEF into the blunted NotI site of the yeast prey vector pVP16-3. Insert can by cut out by XhoI.

6. Transfections, transactivation assays, and yeast two hybrid screens

PC12, COS, HeLa, and HEK293 cells were co-transfected at 50-80% confluency in 6-well plates using Fugene6 (Roche), and 3-5 plasmids (0.1-1.0 µg

25   DNA/well depending on cell types; see plasmid list hereinabove for description of all constructs). All transfections included a. Gal4 (pG5E1B-luc) or LexA (pL8G5-luc) reporter plasmids; b. constitutively expressed β-galactosidase expression plasmid (pCMV-LacZ) to control for transfection efficiency; and c. the Gal4- or LexA-fusion protein vectors. Cells were harvested 48 hr post-transfection in 0.2 ml/well reporter

lysis buffer (Promega), and their luciferase and β-galactosidase activities were
determined with the Promega luciferase assay kit and the O-nitrophenyl-D-galacto-
pyranoside method, respectively. The luciferase activity was standardized by the β-
galactosidase activity to control for transfection efficiency and general effects on

5   transcription, and in most experiments normalized for the transactivation observed in
cells expressing Gal4 or LexA alone. Values shown are averages of transactivation
assays carried out in duplicate, and repeated at least three times for each cell type and
constructs. Most constructs were assayed in three or four cell lines, but usually only
representative results for one cell line are shown. To confirm expression of

10   transfected proteins and secretase cleavage of the various APP constructs, transfected
cells were also analyzed by immunoblotting using antibodies to the respective
proteins and/or antibodies to the epitope tags attached to the proteins.

For assays of the transactivation by Gal4·VP16 constructs, cells were
cotransfected with a. pG5E1B-luc (Gal4 reporter plasmid); b. pCMV-LacZ (ß-

15   galactosidase control plasmid); c. pMst (Gal4), pMst-GV-APP (APP-GV), pMst-GV
(GV), pMst-GV-APPct (APPct-GV), pMst-APPct (APPct-Gal4), pMst-GV-APP*
(APP*-GV), pMst-GV-APPct* (APPct*-GV), pMst-APPct* (APPct*-Gal4), pMst-
GV-APPγ (APPγ-GV), pMst-GV-NRX (NRX-GV), pMst-GV-NA (NRXe-GV-
APPc), or pMst-GV-AN; and d. pcDNA3.1-PS2D366A (kind gift of Dr. C. Haass,

20   Munich), pCMV-Mint1; or pCMV5-Fe65 where indicated.

A yeast two-hybrid cDNA library in pVP16-3 was screened with
pBTM116-APP encoding the cytoplasmic tail of human APP_{695} as described (Vojtek
et al. (1993) Cell 74, 205-214; Okamoto et al. (1997) J. Biol. Chem. 272: 31459-
31464). Of 80 positive clones, 72 encoded Fe65 and one Fe65-like protein. The full-

25   length rat Fe65 sequence has been submitted to GenBank (acc.# AF333983).
Interactions of all proteins including mutants of Fe65 were quantified using liquid ß-
galactosidase assays on yeast strains harboring various bait and prey clones (see
Example 1).

For transactivation by APP-Gal4 and APP-LexA constructs, cells were

30   cotransfected with: a. pG5E1B-luc (Gal4 reporter plasmid) or pL8G5-luc (LexA-
reporter plasmid); b. pCMV-LacZ (ß-galactosidase control plasmid); c. pMst (Gal4),

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pMst-APP (APP-Gal4), pMst-APP* (APP*-Gal4), pMst-APPγ (APPγ-Gal4), pMst-
APPγ* (APPγ*-Gal4), pMst-AN-APPc32 (APP-G-NRX-APPc32), pMst-AN (APPe-
G-NRXc), pML (LexA), pML-APP (APP-LexA), pML-APP* (APP*-LexA), pML-
APPct (APPct-LexA), pML-APPct* (APPct*-LexA); and d. pCMV-Mint1 (mint1) or

5   pCMV5-Fe65 (Fe65) where indicated. Analyses were performed as described above.

COS7 cells were transfected in 100 mm dishes using DEAE-dextran or
Fugene6 (Roche) with single or combinations of expression vectors encoding wild-
type and mutant APPct-Gal4, APPγ-Gal4, and APP-Gal4, myc-tagged or HA-tagged
wild type or mutant Fe65, and wild type and mutant Tip60 (see above for a

10   description of the expression vectors), and harvested 72 hr after transfection. For the
immunoblotting experiments (Fig. 3), cell extracts were immunoblotted with
polyclonal antibodies to the C-terminus of APP (U955) or to Fe65, and with
monoclonal antibodies to Gal4 (Clontech) or to the myc- or HA-epitope (Santa Cruz).
For the immunoprecipitation experiments (Fig. 5), cells were washed twice with cold

15   PBS, harvested in 1 ml lysis buffer (50 mM HEPES-NaOH pH 7.5, 150 mM NaCl,
10% glycerol, 1% IGEPAL CA-630, 1.5 mM MgCl2, 1 mM EGTA, 1 mM DTT, 0.1
g/L PMSF, 10 mg/L Leupeptin, 10 mg/L aprotinin, 1 mg/L pepstatin A), and passed
through a 28 gauge needle 5 x. Cell extracts were clarified by centrifugation at
20,800 x g for 10 min. The supernatants (~1 ml) were incubated with 10 µl of a

20   polyclonal antibody raised against the C-terminus of APP (U955) or monoclonal
antibodies to myc-tag (Santa Cruz) for 2 hr at 4°C, 60 µl of a 50% slurry of protein A-
or protein G-Sepharose (Phamacia) were added, and the beads were incubated with
the reactions for 1 hr at 4°C on a rotator and then collected by centrifugation. Beads
were washed 3 x with lysis buffer, resuspended in 0.1 ml SDS-PAGE sample buffer,

25   and 20 µl of the protein solutions were resolved on 10% SDS-PAGE, and detected by
immunoblotting with antibodies to APP, Gal4, or the myc-epitope.

For transactivation assays of Fe65 mutants, cells were cotransfected
with: a. pG5E1B-luc (Gal4 reporter plasmid) or pL8G5-luc (LexA-reporter plasmid);
b. pCMV-LacZ (ß-galactosidase control plasmid); c. pMst (Gal4), pMst-APP (APP-

30   Gal4), pML (LexA), or pML-APP (APP-LexA); and d. pCMV5-Fe65 (Fe65),
pCMVMyc-Fe65(128-711) (Fe65(128-711)), pCMVMyc-Fe65(242-711) (Fe65(242-

711)), pCMVMyc-Fe65(287-711) (Fe65(287-711)), pCMV5-Fe65(1-553)
(Fe65ΔPTB2), pCMVMyc-Fe65ΔPTB1 (Fe65ΔPTB1), pCMV5-
Fe65mW1(Fe65mW1), pCMV5-Fe65mW2 (Fe65mW2), pCMV5-Fe65mW3
(Fe65mW3), pCMV5-Fe65mW4 (Fe65mW4), or pCMV5-Fe65mW5 (Fe65mW5)

5   where indicated. Analyses were performed as described above, and plasmids are
described above.

Yeast two-hybrid screens were carried out with a fragment from rat
Fe65 (residues 287-711) as described above. Out of 100 clones analyzed, 9 clones
encoded APLP1, and 8 clones Tip60β (residues 63-454 of the insert-minus splice β-

10   variant; submitted to GenBank with acc.# AF333984). The domains of Fe65 that
bind to the cytoplasmic tail of APP or to Tip60 were studied by quantitative yeast
two-hybrid assays which demonstrated that the first PTB domain of Fe65 is necessary
and sufficient for bind to Tip60, and the second PTB domain for binding to APP. For
Tip60, both the partial rat cDNA and the full-length human cDNA were analyzed (see

15   Fig. 6A).

GST-pulldowns were performed essentially as described by Hata et al.
(1993) Nature 366, 347-351 using purified wild type and mutant rat GST-Tip60β and
Fe65 expressed by transfection in COS cells. Extracts from transfected COS cells
were preabsorbed with 10 μg GST on glutathione agarose for 2 hr at 4°C, and then

20   incubated for 4 hrs at 4°C with 10 μg of GST-Tip60, GST-Tip60*, or GST bound to
glutathione agarose. Beads were washed 5 x in lysis buffer, resuspended in 80 μl
SDS-PAGE sample buffer, and 20 μl were analyzed by SDS-PAGE and
immunoblotting using antibodies to Fe65 and to the myc epitope. Co-
immunoprecipitation experiments of Fe65, APP, and wild-type and mutant rat Tip60β

25   were performed as described above using COS cells co-transfected with the
appropriate vectors.

HeLa cells plated on cover glass in a 12-well plate were transfected
with pcDNA3.1-N-HA-Fe65 and pCMVMyc-hTip60 (0.25 μg for each plasmid)
using Fugene6 (Roche). Two days after transfection, cells were washed twice with

30   PBS, fixed (3.7% formaldehyde for 10 min at room temperature), and blocked and
permeabilized in PBS containing 3% BSA, 0.1% IGEPAL CA-630 for 20 min. Cells

were then incubated with anti-HA monoclonal antibody (BAbCO Berkeley antibody

company) and anti-Myc polyclonal antibody (Upstate Biotechnology) for 1 hr (1:200

dilution in blocking buffer), washed with PBS 3 x, and treated with Rhodamine-goat-

anti-mouse and FITC-goat-anti-rabbit antibodies (Chemicom) for 1 hr (1:500 dilution

5   in blocking buffer). After 3 washes with PBS and one wash with water, cells were

mounted and observed with a confocal microscope.

For transactivation assays of Gal4Tip60, COS and HEK293 cells were

cotransfected with: a. pG5E1B-luc (Gal4 reporter plasmid); b. pCMV-LacZ

(β-galactosidase control plasmid); c. pMst (Gal4); pM-Tip60 (rat Gal4-Tip60β

10   residues 63-454); pM-Tip60* (mutant rat Gal4-Tip60β residues 63-454); pM-hTip60

(full-length wild type human Gal4-Tip60β); or pM-hTip60* (full-length mutant

human Gal4-Tip60β) d. pCMV5-Fe65 (Fe65), pCMVMyc-Fe65(242-711) (Fe65(242-

711)), pCMV5-Fe65(1-553) (Fe65ΔPTB2), or pCMV5-Fe65mW4 (Fe65mW4) where

indicated; and e. pCMV5-APP (human APP695) or pCMV5-APP* (mutant human

15   APP695). All transfections contained one of the plasmids listed in a-c, whereas d and

e were variable. Analyses were performed as described above.

<u>Example 2</u>

Nuclear signaling by the cytoplasmic γ-cleavage product of APP

fused to Gal4·VP16. Cleavage of APP produces a C-terminal fragment composed of

20   half of the TMR (10-12 residues) and the cytoplasmic tail (47 residues) (See, e.g.

Selkoe (1998) Trends Cell Biol. 8, 447-453). A transcription factor was engineered

into the cytoplasmic tail of APP. The inserted transcription factor was Gal4·VP16

which is composed of a yeast DNA-binding protein (Gal4) fused to a powerful viral

activator (VP16) (Sadowski et al. (1988) Nature 335, 563-564). When inserted in the

25   cytoplasmic tail of APP, Gal4·VP16 can only act as a transcription factor if APP is

cleaved by γ-secretase, and if the resulting product enters the nucleus. Gal4·VP16

was inserted into full-length APP695 at the cytoplasmic boundary of the TMR, the

resulting APP-Gal4·VP16 fusion protein was transfected into a variety of cell lines

(PC12, HEK293, COS, or HeLa cells), and transactivation of transcription from a co-

30   transfected Gal4-dependent reporter plasmid encoding luciferase was measured.

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Isolated Gal4·VP16 (without APP) was employed as a positive control, and Gal4 alone (without VP16 and APP) as a negative control. In all experiments, cells were co-transfected with a constitutive β-galactosidase expression plasmid in order to control for transfection efficiency, and verified protein expression by immunoblotting.

5   Transfections and analyses were performed as described in Example 1.

Full-length APP-Gal4·VP16 (APP-GV) transactivated Gal4-dependent transcription much stronger than Gal4 alone in all cell types tested (~500-2,000 fold activation depending on cell type). Surprisingly, full-length APP-Gal4·VP16 was as powerful in activating Gal4-dependent transcription as free Gal4·VP16 (GV) without

10   APP (Fig. 1A #1-3). Immunoblotting revealed that the transfected proteins were expressed well, and that APP-Gal4·VP16 was partly cleaved by α- or ß- and γ-secretases in the cells, resulting in stable C-terminal fragments which could be detected by antibodies to Gal4 and to the cytoplasmic tail of APP. A chimeric protein in which Gal4·VP16 was only fused to the cytoplasmic tail of APP without the TMR

15   and extracellular sequences of APP (APPct-GV) was more potent in transactivation than full-length APP-Gal4·VP16, or even Gal4·VP16 alone (~3,000 vs. ~1,000 fold activation; Fig. 1A #5). In contrast, the cytoplasmic APP tail containing only Gal4 without VP16 (APPct-Gal4) was only slightly more active than Gal4 alone (<5 fold activation; Fig. 1A #8). Together these results show that the cytoplasmic tail of APP

20   released by γ-cleavage is competent to enter the nucleus, and may partly activate transcription. Similar results were obtained in all cells tested, and thus are not a unique property of a particular cell line.

To rule out the possibility that transactivation by APP-Gal4·VP16 in transfected cells may be caused by non-specific proteolysis of the APP-Gal4·VP16

25   fusion protein instead of γ-cleavage, the γ-cleavage product of APP with an inserted Gal4·VP16 module in the cytoplasmic tail (APP γ-GV) was directly expressed, and its ability to activate Gal4-dependent transcription was measured (Fig. 1A #6). Similar to the cytoplasmic tail fragment of APP, the isolated γ-cleavage product was more active in transcription than full-length APP-Gal4·VP16 or Gal4·VP16 alone,

30   confirming that the hydrophobic residues in the γ-cleavage product do not inhibit transactivation.

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<u>Example 3</u>

Sequence-specificity of transactivation mediated by APP-

Gal4·VP16. The cytoplasmic tail of APP contains a conserved NPTY sequence that

constitutes a binding site for the PTB-domains of at least three proteins, Fe65,

5   Mints/X11s, and Disabled (Fiore et al. (1995) J. Biol. Chem. 270, 30853-30856;

McLoughlin et al. FEBS Lett. 397, 197-200; Borg et al. (1996) Mol. Cell. Biol. 16,

6229-6241). Binding of these proteins to APP could contribute to the transcriptional

activation mediated by APP-Gal4·VP16 by influencing γ-cleavage of APP, or by

participating in nuclear translocation. This possibility was examined by mutating the

10   NPTY sequence in the cytoplasmic tail of APP to NATA. Transactivation assays

showed that in all cell types tested, the NPTY-mutants of Gal4·VP16 fusion proteins

were as potent as wild type proteins in activating transcription (Fig. 1A #4, 7 & 9),

suggesting that the NPTY motif and its binding proteins are not essential for

transactivation by the Gal4·VP16 module inserted into APP. In agreement with this

15   conclusion, co-transfection of Fe65 did not cause a major change in transactivation by

APP-Gal4·VP16.

        The specificity of transactivation by Gal4·VP16 inserted into a

membrane protein was examined by introducing Gal4·VP16 into the cytoplasmic tail

of neurexin 1β as a control protein that is also expressed on the neuronal cell-surface

20   but is not known to be processed by proteolytic cleavage (Ushkaryov et al. (1992)

Science 257, 50-56). Neurexin 1β-Gal4·VP16 (NRX-GV) did not exhibit

transactivation in contrast to APP-Gal4·VP16 (Fig. 1B, #3 & 10), suggesting that not

all cell-surface Gal4·VP16-fusion proteins are competent for transactivation. In these

experiments, a dominant negative mutant of presenilin 2 (Steiner et al. (1999) J. Biol.

25   Chem. 274, 28669-28673) was co-transfected with the Gal4·VP16-fusion proteins to

test if presenilins are involved. As expected, transactivation by full-length APP-

Gal4·VP16 was inhibited by the presenilin 2 mutant, whereas the small amount of

residual transactivation observed with neurexin 1ß-Gal4·VP16 was insensitive to

presenilin 2 (Fig. 1B, #3 & 10).

30   To determine which APP sequences enable the inserted Gal4·VP16 to

activate transcription, chimeric proteins containing different combinations of the

extracellular and intracellular sequences of APP and of neurexin 1β were produced.
When extracellular sequences and TMR of APP were fused to Gal4·VP16 and to the
cytoplasmic tail of neurexin 1ß (APPe-GV-NRXc), potent transactivation was
observed. In contrast, the reverse fusion protein of the extracellular domain and TMR

5   of neurexin 1ß with the cytoplasmic tail of APP (NRXe-GV-APPc) was inactive (Fig.
1B, #11 and 12). Again, presenilin 2 inhibited the chimeric protein containing the
extracellular domain of APP but had no effect on the residual transactivation observed
with the protein containing the extracellular domain of neurexin 1β, supporting the
notion that specific APP-sequences are required for transactivation as studied by this

10   assay.

Example 4

**Fe65 binding to the cytoplasmic tail of APP stimulates
transcription.** To identify co-factors that may be involved in nuclear signaling with
the cytoplasmic tail of APP, yeast two-hybrid screens for proteins that bind to the

15   cytoplasmic tail of APP were performed as described in Example 1. Similar to
previous screens (26-31), Fe65 was the major interacting protein identified, although
it was isolated at an unexpectedly high frequency (90% of all clones).

A further assay was performed to determine whether Fe65 represents a
co-factor for APP in nuclear signaling. Without Fe65, APP-Gal4 activated Gal4-

20   dependent transcription only weakly (<10 fold). By contrast, co-expression of Fe65
with APP-Gal4 powerfully stimulated transcription (200-2,000 fold depending on the
cell type). This was observed in all cell lines tested (PC12, HEK293, COS, or HeLa
cells) (Fig. 2A-2C). As a control, co-expression of mint 1/X11 which also binds to
the cytoplasmic tail of APP (See, e.g., Fiore et al. (1995) J. Biol. Chem. 270; 30853-

25   30856), had no major effect on transactivation under these conditions. Neither Fe65
nor mint1/X11 changed the transcription of the control ß-galactosidase plasmid co-
transfected into all cells.

To examine whether Fe65 still stimulates transactivation when the
Fe65-binding site in the cytoplasmic tail of APP (the NPTY sequence) is mutated,

30   yeast two hybrid assays and co-immunoprecipitations were performed as described in
Example 1. Replacing the NPTY sequence with NATA abolished Fe65 binding as

shown by yeast two-hybrid assays and co-immunoprecipitations (see also Fig. 5
below). In agreement with a direct role for Fe65 binding in stimulating
transactivation by the cytoplasmic tail of APP, the same mutation also abolished the
Fe65-dependent stimulation of transcription (Fig. 2A).   '

5   The hypothesis that Fe65 binds to the cytoplasmic γ-cleavage product
of APP to activate Gal4-dependent transcription in the nucleus was confirmed by the
observation that Fe65 powerfully stimulated transactivation by a "precleaved" APP-
Gal4 fragment corresponding to the γ-cleavage product (200-2,000 fold stimulation of
transactivation depending on cell type; Fig. 2B). The effect of Fe65 depended on the
10   intact Fe65-binding site in the cytoplasmic tail of APP (Fig. 2B). The relative activity
of APP-Gal4 co-transfected with Fe65 compares well to that of the potent Gal4·VP16
fusion protein, suggesting that Fe65 is a powerful transcriptional activator. Further
evidence for the notion that Fe65 needs to bind to the cytoplasmic APP tail in order to
stimulate transcription was obtained with series of chimeric APP/neurexin constructs
15   (Fig. 2C). When the cytoplasmic tail of APP-Gal4 was replaced with the cytoplasmic
tail of neurexin 1ß, Fe65 did not stimulate transactivation. However, when the 32
amino acid Fe65-binding site from the cytoplasmic tail of APP was transplanted into
the middle of the neurexin cytoplasmic tail, powerful stimulation of transcription
(>200 fold over Gal4) was observed (Fig. 2C).

20   To ensure that APP-Gal4 is indeed cleaved at the γ-secretase site in the
transfected cells, the size of the APP-Gal4 cleavage products was examined. COS
cells were transfected with Gal4-fusion proteins of full-length APP (as test protein),
and of the cytoplasmic tail and the γ-cleavage product of APP (as size standards to
identify the correct cleavage product) as described above. Immunoblotting of the
25   transfected cells with antibodies to the cytoplasmic tail of APP and to Gal4 detected
two major APP cleavage products (Fig. 3). A fragment that was bigger than the γ-
cleavage product, tentatively identified as the   - or ß-secretase product, and a
fragment that of precisely the same size as the γ-cleavage product but slightly larger
than the cytoplasmic tail protein alone (Fig. 3) were detected. No artifactual cleavage
30   at the boundary of the TMR and the inserted Gal4 protein was detected, while the γ-
secretase cleavage product was abundantly produced. Furthermore, analyses of cells

co-transfected with Fe65 revealed that Fe65 had no apparent effect on the production
of the α- and γ-cleavage products.

Example 5

**Fe65 stimulates transactivation independent of the DNA binding
5   protein.** Gal4 contains an intrinsic nuclear localization signal (Silver et al. (1984)
Proc. Natl. Acad. Sci. USA 81, 5951-5955) and theoretically could cause non-specific
transcriptional activation that could be unrelated to the normal functions of these
proteins. To exclude Gal4-specific artifacts, APP was fused to the bacterial LexA
DNA-binding protein (Smith et al. (1988) EMBO J. 7, 3975-3982), and measured
10   Fe65-dependent transactivation with a LexA-dependent luciferase reporter as
described in Example 3 (Fig. 4). In the absence of Fe65, APP-LexA did not mediate
significant transactivation (Fig.4B). However, co-transfection of Fe65 strongly
stimulated transactivation (40-100 fold). The effect of Fe65 was less pronounced
with LexA than with Gal4, possibly because the bacterial LexA DNA-binding domain
15   acting on a bacterial promoter sequence is less optimal for mammalian transcription.
Similar to the Gal4 system, however, Fe65 stimulated transactivation both with full-
length APP and with the isolated cytoplasmic tail, and stimulation depended on the
intact Fe65-binding site in the cytoplasmic tail of APP.

Example 6

20   **The WW-domain and both PTB-domains of Fe65 are required for
transactivation.** Fe65 is a multidomain protein that contains a negatively charged N-
terminal sequence with no homology to other proteins, a central WW-domain, and
two C-terminal PTB-domains (Ermekova et al. (1998) Adv. Exp. Med. Biol. 446,
161-180; McLoughlin et al. (1998) Biochem. Soc. Trans. 26, 497-500). The WW-
25   domain of Fe65 interacts with the cytoskeletal adaptor protein mena (Ermekova et al.
(1997) J. Biol. Chem. 272, 32869-32877). The second PTB-domain of Fe65 (PTB2)
binds to the cytoplasmic tails of APP and other cell-surface proteins containing NPxY
motifs (Fiore et al. (1995) J. Biol. Chem. 270: 30853-30856). In addition to these
cytoplasmic activities, Fe65 has been implicated in nuclear functions. Fe65 is partly
30   localized to the nucleus, its first PTB-domain (PTB1) binds to the transcription factor

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CP2/LSF/LBP1, and its negatively charged N-terminal sequences stimulates Gal4-dependent transcription (Duilio et al. (1991) Nucleic Acids Res. 19, 5269-5274). The foregoing data establish that the γ-cleavage product of APP forms a complex with Fe65 that transactivates a heterologous promoter, suggesting that the APP/ Fe65

5   complex functions as a transcriptional activator.

To investigate how the APP/Fe65 complex activates transcription, a series of Fe65 deletion mutants were constructed and their ability to stimulate transactivation was determined as described in Example 1. Both APP-Gal4 and APP-LexA were used to ensure that the effects observed were not peculiar to a particular

10   DNA-binding protein (Fig. 5). The WW-domain and both PTB-domains of Fe65 were found to be essential for activating transcription. By contrast, deletion of the N-terminal third of Fe65 with the acidic region suspected of activating transcription had no effect on transactivation (Figs. 5A and 5B). The results indicate that in addition to the binding of the second PTB domain of Fe65 to the cytoplasmic tail of APP, the

15   WW-domain and the first PTB domain also interact with target molecules in order for Fe65 to stimulate transcription.

The Fe65 deletion mutants suggest that Fe65 is a true adaptor protein in transcriptional regulation. To exclude possible artifacts induced by the deletions, immunoblotting was performed to confirm that all of the transfected proteins were

20   stably expressed, and not prematurely degraded. Immunoprecipitations from COS cells which co-express wild type or mutant Fe65 and APP-Gal4 showed that deletion of the first PTB-domain in Fe65 does not impair its ability to bind to the cytoplasmic tail of APP as long as that tail contains a wild type NPTY sequence (Fig. 5C and 5D). Finally, point mutations in the WW-domain were used instead of a large deletion to

25   assess the need for the WW domain in the stimulation of transactivation. Substitution of one of the conserved tryptophan residues of the WW-domain had no effect, while replacement of the central YYW motif with alanine residues abolished the Fe65-dependent stimulation of transcription (Figs. 5A and 5B). Again, immunoblotting confirmed that all mutants were stably expressed, and none of the Fe65 proteins

30   influenced basal transcription from the co-transfected control plasmids. Together these experiments show that all three canonical domains of Fe65 are required to

activate transcription in a complex with the cytoplasmic tail of APP, establishing that
Fe65 is a genuine adaptor protein which links multiple components into a single
active complex.

Example 7

5   **Fe65 binds to the histone acetyl transferase Tip60.** As an adaptor
protein, Fe65 presumably directly or indirectly interacts with transcription factors
when it activates transcription. A candidate for such a binding protein is the
transcription factor LBP/CP2/LSF which interacts with the first PTB-domain of Fe65
(Duilio et al. (1991) Nucleic Acids Res. 19, 5269-5274). However, only a weak

10   interaction between LBP/CP2/LSF and Fe65 was observed in quantitative yeast two-
hybrid assays, and no change in the amount of transactivation was detected when
LBP/CP2/LSF was co-transfected with Fe65 and APP-Gal4. Other Fe65-interacting
proteins were searched for using yeast two-hybrid screens as described in Example 1.
A single prey clone that strongly bound to the first PTB-domain of Fe65, and that

15   contains almost the entire coding sequence for Tip60, was identified. Tip60 is a
histone acetyl transferase that is expressed in two alternatively spliced forms (Tip60α
and β), interacts with multiple transcription factors, and is part of a large complex in
the nucleus (Kamine et al. (1996) Virology 216, 357-366). Quantitative yeast two-
hybrid assays, GST-pulldown studies, and co-immunoprecipitation experiments

20   confirmed a strong interaction of Fe65 with both the partial rat Tip60ß obtained in the
yeast two-hybrid screens, and with full-length human Tip60β (Figs. 6A and 6B).
Furthermore, immunofluorescence analyses of transfected cells showed that Fe65 and
Tip60ß colocalize in the nucleus in a speckled pattern, suggesting that they function
as a complex (Figs. 6C-6F).

25   PTB-domains usually bind to NPxY target sequences, although variant
binding sequences have also been observed (Zwahlen et al. (2000) EMBO J. 19,
15005-15015). In a search for a possible PTB-domain target sequence in Tip60, a
single motif was detected that is remotely similar to the NPxY sequence (NKSY;
residues 257-260). Mapping of the NKSY sequence onto the three-dimensional

30   structure of Esa1, a yeast histone acetyl-transferase whose three-dimensional structure
has been solved (Yan et al. (2000) *Mol. Cell* 6, 1195-1205), suggests that the NKSY

motif in Tip60 is located on a surface loop of a conserved domain, and thus accessible for a binding partner. To test if the Fe65 PTB1-domain binds to this site, the Tip60 NKSY sequence was mutated into NASA, and the ability of mutant Tip60 to bind to Fe65 was tested. No binding was observed for the mutant as measured either by

5   quantitative yeast two-hybrid assays or GST-pulldowns (Fig. 6A and 6B), suggesting that the first PTB-domain of Fe65 binds to the NKSY sequence in Tip60.

Example 8

Binding of the APP/Fe65 complex to Tip60 mediates

transactivation. To test if Fe65 enhances transactivation by binding to the Tip60

10   complex, a Gal4-Tip60 fusion protein was constructed, and the effects of Fe65 and APP on Gal4-dependent transactivation mediated by the Gal4-Tip60 fusion protein were examined(Fig. 7). Gal4-Tip60 alone was unable to support significant Gal4-dependent transcription (no activation over Gal4 alone). Co-expression of either Fe65 . or APP individually with Gal4-Tip60 did not enhance transactivation. However,

15   when Gal4-Tip60 was co-expressed with both Fe65 and APP, transactivation was stimulated dramatically (~100 fold; Fig. 7). Mutant APP that is unable to bind to Fe65 (APP*) was largely inactive (~10 fold enhancement of transactivation). Furthermore, no potentiation of transactivation was observed when Fe65 and APP were co-expressed with mutant Gal4-Tip60 (Gal4-Tip60*) that is unable to bind to

20   Fe65, or with Gal4 only. Together these data show that the cytoplasmic tail of APP has a direct active role in stimulating transactivation, and that it collaborates with Fe65 in enhancing transcription by Gal4-Tip60.

In experiments described above (Fig. 5), it was found that all three canonical Fe65 domains (the WW domain and the two PTB domains) are required for

25   Fe65 to potentiate transactivation by Gal4- and LexA-APP proteins. In order to test if the same applies for the Fe65- and APP-dependent transactivation by Gal4-Tip60, a series of Fe65 mutants was examined in this assay (Fig. 7). The N-terminal sequence of Fe65 was not needed for potentiating Gal4-Tip60 dependent transactivation, whereas the second PTB-domain that binds to APP was essential. The WW domain

30   of Fe65 was also found to be indispensable.

The foregoing data provide a model for the function of APP and its homologs whereby proteolytic cleavage of APP releases the cytoplasmic tail to activate a nuclear signal in transcription (Fig. 8).

All references cited herein are incorporated herein in their entirety.

CLAIMS

1.   A method of identifying an agent that affects the cleavage of
amyloid-β precursor protein (APP) comprising providing a cell containing APP
modified in the C-terminal cytoplasmic tail to allow detection of nuclear localization
of said cytoplasmic tail; contacting said cell with a candidate agent; and measuring
5   nuclear localization of said C-terminal cytoplasmic tail, wherein an increase or
decrease in nuclear localization in the presence of said candidate agent relative to
nuclear localization in the absence of said candidate agent is indicative of an agent
that affects the cleavage of APP.

2.   The method of Claim 1 wherein APP is modified to comprise a
10   DNA-binding domain of a transcription factor and a transcriptional activator of the
same or a different transcription factor, and wherein said cell further contains an
indicator gene operably linked to a nucleic acid comprising a binding site for said
DNA-binding domain.

3.   The method of Claim 2 wherein said DNA-binding domain is
15   Gal4 or LexA.

4.   The method of Claim 2 wherein said transcriptional activator is
VP16.

5.   The method of Claim 1 wherein said APP is modified to
comprise a DNA-binding domain of a transcription factor and wherein said cell
20   further comprises an indicator gene operably linked to a nucleic acid comprising a
binding site for said DNA-binding domain, and wherein Fe65 is provided to said cell.

6.   The method of Claim 5 wherein said DNA-binding domain is
Gal4 or LexA.

7.   The method of Claim 2 wherein nuclear localization is measured by measuring expression of said indicator gene.

8.   The method of Claim 5 wherein nuclear localization is measured by measuring expression of said indicator gene.

5   9.   The method of Claim 1 wherein said cell is a eukaryotic cell.

10.   The method of Claim 1 wherein said cell is a mammalian cell.

11.   The method of Claim 1 wherein said cell is a human cell.

12.   A method of identifying an agent that affects the cleavage of amyloid-β precursor protein (APP) comprising co-transfecting a cell with (a) a nucleic

10   acid encoding a modified APP, wherein said modified APP comprises Gal4 and VP16 in the C-terminal cytoplasmic tail, and (b) a nucleic acid encoding an indicator gene under the control of one or more copies of a Gal4 regulatory element; contacting said cell with a candidate agent; and measuring expression of said indicator gene, wherein an increase or decrease in expression in the presence of said candidate agent relative

15   to the absence of said agent is indicative of an agent that affects cleavage of APP.

13.   A method of identifying an agent that affects the cleavage of amyloid-β precursor protein (APP) comprising providing a cell containing APP and Tip60 modified to allow detection of nuclear localization of a C-terminal cytoplasmic cleavage product of APP; contacting said cell with a candidate agent; and measuring

20   nuclear localization of said C-terminal cytoplasmic cleavage product, wherein an increase or decrease in nuclear localization in the presence of said agent relative to nuclear localization in the absence of said agent is indicative of an agent that affects the cleavage of APP.

14.   The method of Claim 13 wherein said Tip60 is modified by fusion with the DNA binding domain of a transcriptional activator, and wherein said cell further contains Fe65.

15.   The method of Claim 14 wherein said DNA binding domain is
5   Gal4 or LexA.

16.   The method of Claim 14 wherein said cell further contains an indicator gene operably linked to a nucleic acid comprising a binding site for said DNA binding domain.

17.   The method of Claim 16 wherein said nuclear localization is
10   measured by measuring expression of said indicator gene.

18.   The method of Claim 13 wherein said cell is a eukaryotic cell.

19.   The method of Claim 13 wherein said cell is a mammalian cell.

20.   The method of Claim 13 wherein said cell is a human cell.

21.   A method of identifying an agent that affects the cleavage of
15   amyloid-β precursor protein (APP) comprising co-transfecting a cell with (a) a nucleic acid encoding APP, (b) a nucleic acid encoding Fe65, (c) a nucleic acid encoding a fusion protein of Tip60 and Gal4, and (d) a nucleic acid encoding an indicator gene under the control of one or more copies of a Gal4 regulatory element; contacting said cell with a candidate agent; and measuring expression of said indicator gene, wherein
20   an increase or decrease in expression in the presence of said candidate agent relative to the absence of said agent is indicative of an agent that affects the cleavage of APP.

22.   A vector comprising a first nucleic acid encoding amyloid-β precursor protein (APP) operably linked to a promoter, wherein a second nucleic acid encoding a heterologous DNA-binding domain of a transcription factor is contained

within the region of the first nucleic acid that encodes the C-terminal cytoplasmic tail of APP.

23.   A vector comprising a nucleic acid encoding amyloid-β precursor protein (APP) operably linked to a promoter wherein a nucleic acid module

5   encoding a heterologous DNA-binding domain of a transcription factor and a transcriptional activator of the same or a different transcription factor is contained within the region of the nucleic acid that encodes the C-terminal cytoplasmic tail of APP.

24.   The vector of Claim 28 wherein the DNA-binding domain is

10   Gal4 or LexA.

25.   The vector of Claim 23 wherein the DNA-binding domain is Gal4 or LexA and the transcriptional activator is VP16.

26.   A vector comprising a nucleic acid encoding Tip60 and a heterologous DNA binding domain of a transcription factor.

15   .   27.   The vector of Claim 26 wherein said DNA binding domain is Gal4.

28.   A cell comprising the vector of Claim 22.

29.   A cell comprising the vector of Claim 23.

30.   A cell comprising the vector of Claim 24.

20   31.   An agent that affects the cleavage of amyloid-β precursor protein (APP) identified by a method comprising providing a cell containing APP modified in the C-terminal cytoplasmic tail to allow detection of nuclear localization of said cytoplasmic tail; contacting said cell with a candidate agent; and measuring

nuclear localization of said C-terminal cytoplasmic tail, wherein an increase or decrease in nuclear localization in the presence of said candidate agent relative to nuclear localization in the absence of said candidate agent is indicative of an agent that affects the cleavage of APP.

5   32.   An agent that affects the cleavage of amyloid-β precursor protein (APP) identified by a method comprising providing a cell containing APP and a protein that interacts with APP to activate transcription, wherein the protein is modified to allow detection of nuclear localization of a C-terminal cytoplasmic cleavage product of APP; contacting said cell with a candidate agent; and measuring

10   nuclear localization of said C-terminal cytoplasmic cleavage product, wherein an increase or decrease in nuclear localization in the presence of said agent relative to nuclear localization in the absence of said agent is indicative of an agent that affects the cleavage of APP.

33.   A composition comprising the agent of Claim 31.

15   34.   A composition comprising the agent of Claim 32.

35.   A kit comprising a first compartment containing cells comprising a vector wherein said vector comprises a nucleic acid encoding amyloid-β precursor protein (APP) operably linked to a promoter wherein a nucleic acid module encoding a heterologous DNA-binding domain of a transcription factor and a

20   transcriptional activator of the same or a different transcription factor is contained within the region of the nucleic acid that encodes the C-terminal cytoplasmic tail of APP.

36.   The kit of Claim 35 wherein said cells further contain a nucleic acid encoding an indicator gene under the control of a regulatory element for said

25   DNA-binding domain.

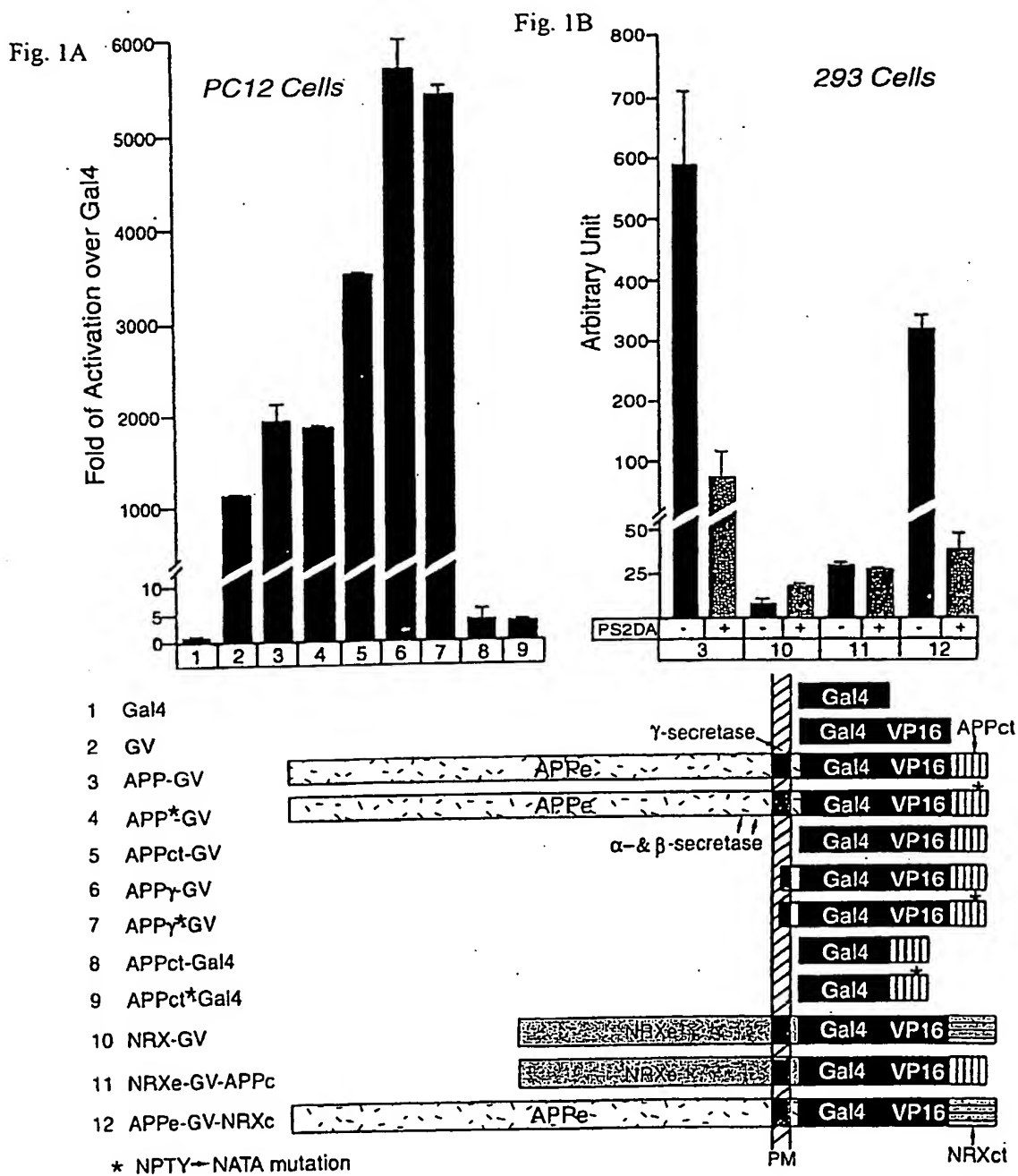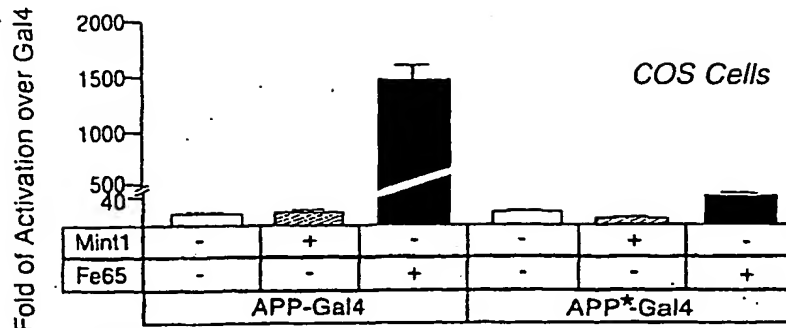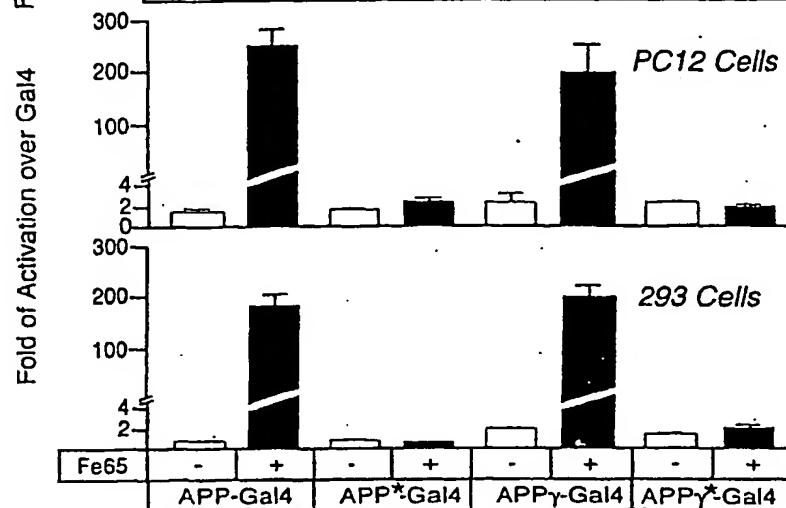37.   A kit comprising a first compartment containing a vector comprising a nucleic acid encoding amyloid-β precursor protein (APP) operably linked to a promoter wherein a nucleic acid module encoding a heterologous DNA-binding domain of a transcription factor and a transcriptional activator of the same or

5   a different transcription factor is contained within the region of the nucleic acid that encodes the C-terminal cytoplasmic tail of APP.

38.   The kit of Claim 37 further comprising a second compartment containing a reporter plasmid comprising a nucleic acid encoding an indicator gene under the control of a regulatory element for said DNA-binding domain.

Fig. 1A
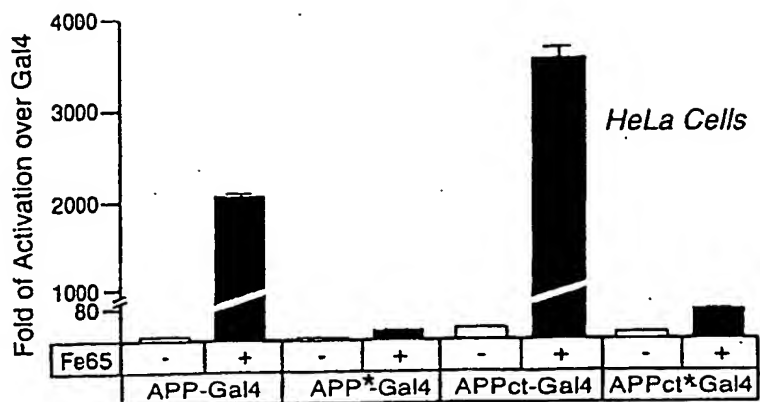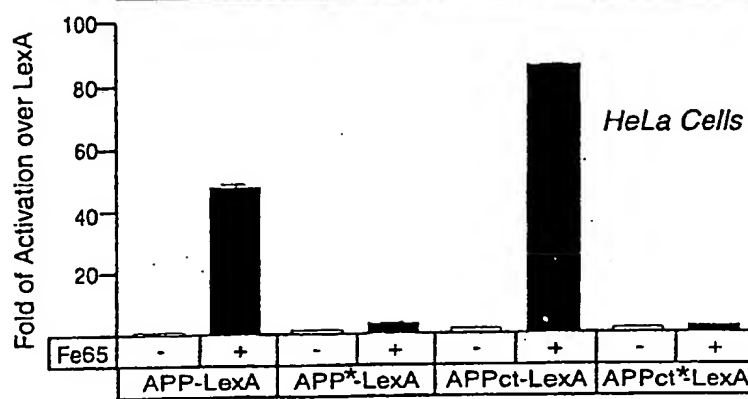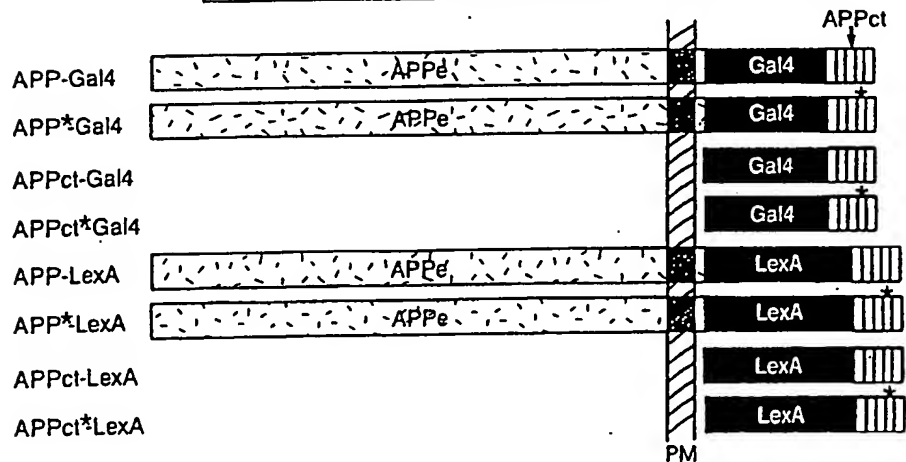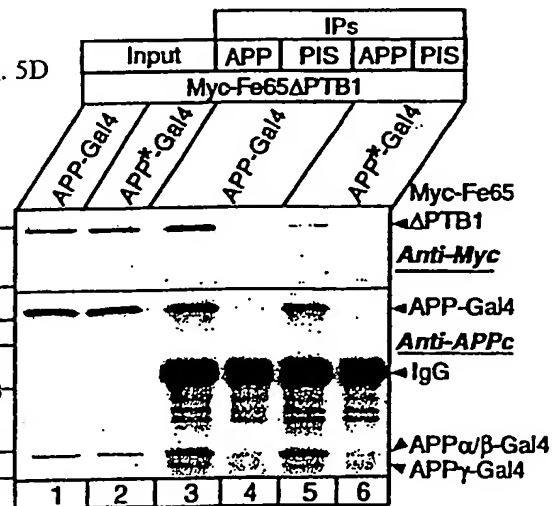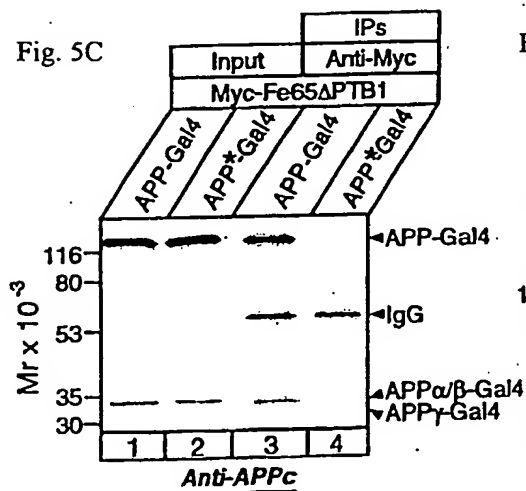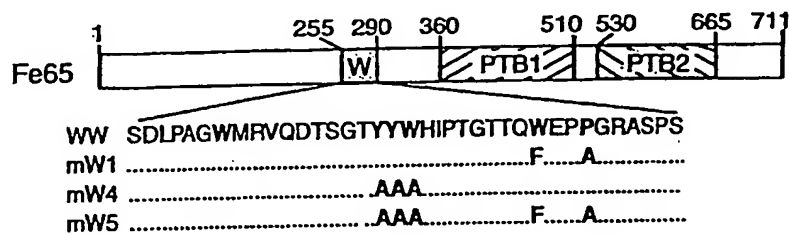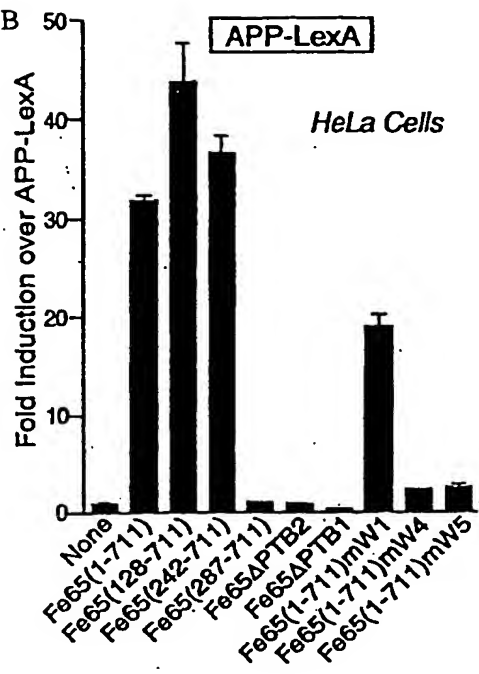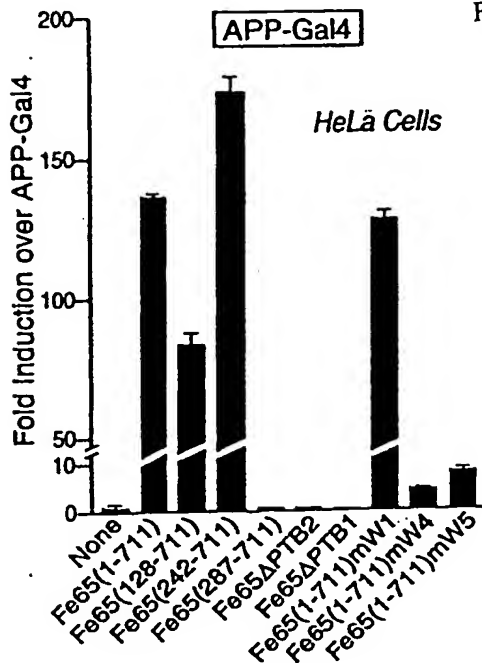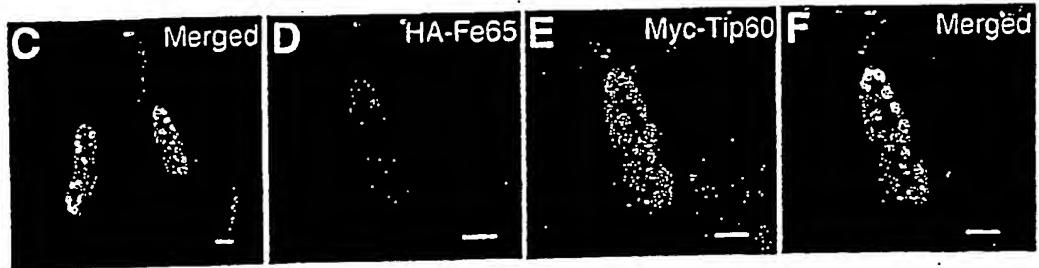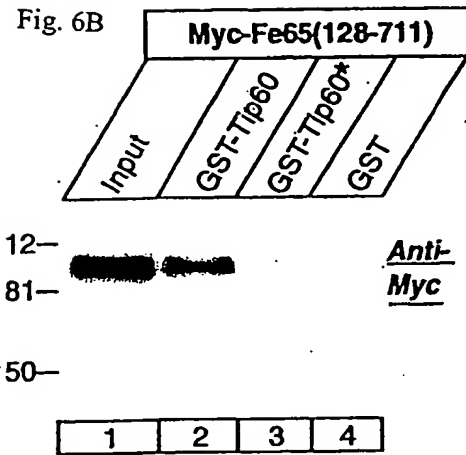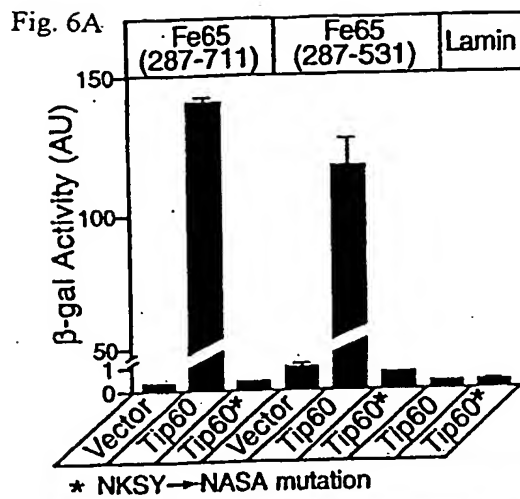
Fig. 1B

Fig. 1C

Fig. 2A

COS Cells

Mint1	-	+	-	-	+	-
Fe65	-	-	+	-	-	+
	APP-Gal4			APP*-Gal4		

Fig. 2B

PC12 Cells

293 Cells

| Fe65 | - | + | - | + | - | + | - | + |
| | APP-Gal4 | | APP*-Gal4 | | APPγ-Gal4 | | APPγ*-Gal4 | |

Fig. 2C

COS Cells

| Fe65 | - | + | - | + | - | + |
| | APP-Gal4 | | APP-G-NRX-APPc32 | | APPe-G-NRXc | |

Fig. 2D

APP-Gal4
APP*-Gal4
APPγ-Gal4
APPγ*-Gal4
APP-G-NRX-APPc32
APPe-G-NRXc

* NPTY → NATA mutation

Fig. 3

Fig 4A

Fig. 4B

Fig. 4C

Fig. 5A
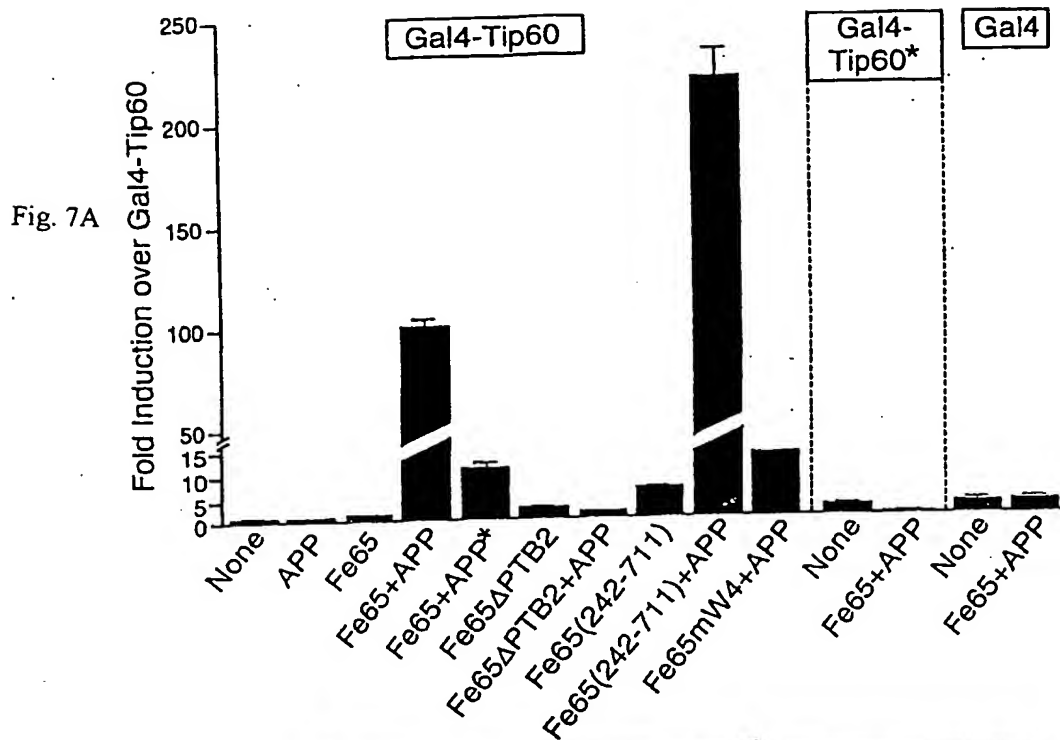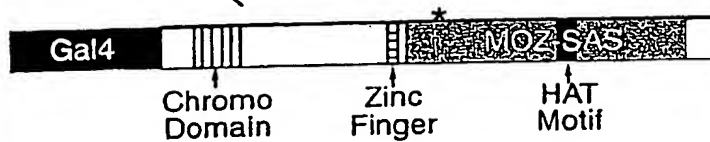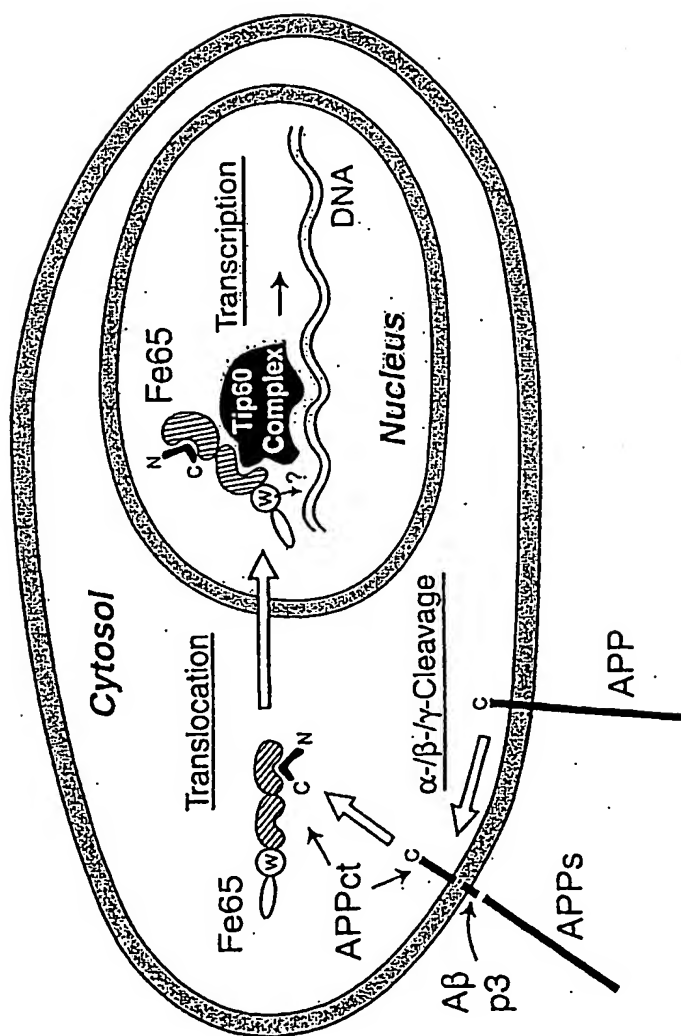
Fig. 5B

Fig. 5E

Fig. 5C

Fig. 5D

Fig. 6A

Fe65 (287-711)			Fe65 (287-531)			Lamin	

β-gal Activity (AU)

150—

100—

50—
1—
0—

Vector | Tip60 | Tip60* | Vector | Tip60 | Tip60* | Tip60 | Tip60*

* NKSY→NASA mutation

Fig. 6B

Myc-Fe65(128-711)			
Input	GST-Tip60	GST-Tip60*	GST

$Mr \times 10^{-3}$

112—
81—

50—

Anti-Myc

1	2	3	4

C   Merged

Fig. 6C

D   HA-Fe65

Fig. 6D

E   Myc-Tip60

Fig. 6E

F   Merged

Fig. 6F

Fig. 7A

Fig. 7B

Fig. 8

INTERNATIONAL SEARCH REPORT

A.	CLASSIFICATION OF SUBJECT MATTER
IPC(7)	: C12Q 1/37; C07K 1/00, 14/47; C07H 21/02, 21/04; C12N 1/14, 5/02, 9/50
US CL	: 435/23, 219, 212, 395, 254.2, 325; 530/350; 536/23.1, 23.4

According to International Patent Classification (IPC) or to both national classification and IPC

B.	FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 435/23, 219, 212, 395, 254.2, 325; 530/350; 536/23.1, 23.4

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
MEDLINE, BIOSIS, EMBASE, CAPLUS

C.	DOCUMENTS CONSIDERED TO BE RELEVANT	
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 00/34511 A2 (AVENTIS PHARMA DEUTSCHLAND GMBH), 15 June 2000	1-21
---	(15.06.00). Abstract, claims 1, 3 and 20.	---------
Y		22-38
Y, P	US 6,333,167 B1 (QUINET et al.) 25 December 2001, claims 1, 8 and 20.	1-38

☐ Further documents are listed in the continuation of Box C.   ☐ See patent family annex.

*	Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"A"	document defining the general state of the art which is not considered to be of particular relevance	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"E"	earlier application or patent published on or after the international filing date		
"L"	document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"O"	document referring to an oral disclosure, use, exhibition or other means		
"P"	document published prior to the international filing date but later than the priority date claimed	"&"	document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
21 July 2002 (21.07.2002)	0 9 SEP 2002

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